

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 17, 2003, 18:19:29 ; Search time 54 Seconds
(without alignments)
824.721 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MEFSLLPRLPCNGAISAHR.....FIRGVSPLYSGNSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	100.0	375	US-09-964-666-2	Sequence 2, Appli
2	2034	100.0	375	US-09-964-412-2	Sequence 2, Appli
3	2034	100.0	375	US-09-964-667-2	Sequence 2, Appli
4	2034	100.0	375	US-09-872-968-2	Sequence 2, Appli
5	2034	100.0	375	US-10-146-130-2	Sequence 2, Appli
6	2034	100.0	375	US-10-092-934-10	Sequence 10, Appli
7	2034	100.0	375	US-10-153-334-1	Sequence 1, Appli
8	2034	100.0	375	US-10-198-069-1	Sequence 1, Appli
9	2034	100.0	375	US-10-157-031-299	Sequence 299, App
10	2034	100.0	375	US-10-198-070-1	Sequence 1, Appli
11	734.5	36.1	361	US-09-995-494-107	Sequence 107, App
12	729	35.8	449	US-10-007-280A-140	Sequence 140, App
13	428.5	21.1	183	US-09-989-920-245	Sequence 245, App
14	382.5	18.8	673	US-10-157-031-291	Sequence 291, App
15	332	16.3	108	US-10-078-090-143	Sequence 143, App
16	316	15.5	152	US-10-198-070-112	Sequence 112, App

17	308	15.1	93	US-09-764-891-5337	Sequence 5337, Ap
18	308	15.1	93	US-10-205-428-486	Sequence 486, App
19	308	15.1	100	US-10-015-157A-187	Sequence 187, App
20	294.5	14.5	92	US-10-198-070-51	Sequence 51, Appl
21	281.5	13.8	115	US-09-995-494-79	Sequence 79, Appl
22	276	13.6	122	US-09-764-847-869	Sequence 869, Appl
23	276	13.6	122	US-10-092-154-869	Sequence 869, App
24	275	13.5	105	US-09-989-919-121	Sequence 121, App
25	273.5	13.4	118	US-10-198-070-30	Sequence 30, Appl
26	270	13.3	126	US-10-082-830-207	Sequence 207, App
27	264	13.0	91	US-10-001-857-198	Sequence 198, App
28	263	12.9	48	US-10-153-334-48	Sequence 48, Appl
29	262	12.9	118	US-10-198-070-116	Sequence 116, App
30	261	12.8	66	US-10-198-070-61	Sequence 61, Appl
31	260.5	12.8	109	US-09-989-919-105	Sequence 105, App
32	259	12.7	172	US-09-764-864-1058	Sequence 1058, Ap
33	259	12.7	232	US-10-198-070-34	Sequence 34, Appl
34	254.5	12.5	239	US-09-800-729-193	Sequence 193, App
35	254.5	12.5	239	US-10-198-070-113	Sequence 113, App
36	254.5	12.5	310	US-09-800-729-190	Sequence 190, App
37	254	12.5	147	US-09-764-891-3556	Sequence 3556, Ap
38	253	12.4	171	US-10-198-070-39	Sequence 39, Appl
39	251.5	12.4	91	US-10-011-585A-156	Sequence 156, App
40	251.5	12.4	144	US-10-011-585A-145	Sequence 145, App
41	251	12.3	776	US-10-020-079-24	Sequence 24, Appl
42	251	12.3	789	US-10-020-079-22	Sequence 22, Appl
43	251	12.3	863	US-10-020-079-32	Sequence 32, Appl
44	251	12.3	876	US-10-020-079-30	Sequence 30, Appl
45	251	12.3	889	US-10-020-079-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-964-666-2
; Sequence 2, Application US/09964666
; Patent No. US20020104108A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Wands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,666
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-666-2

Query Match 100.0%; Score 2034; DB 11; Length 375;
Best Local Similarity 100.0%; Pred. No. 3,9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLPRLCNGAISAHRNRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
DB 1 MEFSLLPRLCNGAISAHRNRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
QY 61 LHVQAGLELPTSDPSVASQSARVYRTGHHARCLANFCGRNRYSLMCPSPSELKOST 120
DB 61 LHVQAGLELPTSDPSVASQSARVYRTGHHARCLANFCGRNRYSLMCPSPSELKOST 120
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DB 121 CLSLPKCWDYRAAHPGLIFLFLRHRCPTLTODEVQWCHSSLOPSTPEIKHPPASASQ 180
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DB 181 VAGTRDMHHTWLIJFIENFLRQSLNSVTQAGVQWRNLGSLQPLPFGFKLFSCPSLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGCDLPASASQAGITGVSHHARLIENFC 300
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QY 301 LFEHESHVTOAGVQWPNLGSLOPLPGLKRFSCSLPSSWDYGHLPHPANFCIFIRG 360
DB 301 LFEHESHVTOAGVQWPNLGSLOPLPGLKRFSCSLPSSWDYGHLPHPANFCIFIRG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 2

US-09-964-412-2
Sequence 2, Application US/09964412
Patent No. US20020129391A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
Wands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,412

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609,4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-412-2

Query Match 100.0%; Score 2034; DB 11; Length 375;
Best Local Similarity 100.0%; Pred. No. 3,9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLPRLCNGAISAHRNRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
DB 1 MEFSLLPRLCNGAISAHRNRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
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DB 61 LHVQAGLELPTSDPSVASQSARVYRTGHHARCLANFCGRNRYSLMCPSPSELKOST 120
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DB 121 CLSLPKCWDYRAAHPGLIFLFLRHRCPTLTODEVQWCHSSLOPSTPEIKHPPASASQ 180
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DB 181 VAGTRDMHHTWLIJFIENFLRQSLNSVTQAGVQWRNLGSLQPLPFGFKLFSCPSLSS 240
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DB 241 WDYRRPRLANFVFLVEMGFTMFARLLISGCDLPASASQAGITGVSHHARLIENFC 300
QY 301 LFEHESHVTOAGVQWPNLGSLOPLPGLKRFSCSLPSSWDYGHLPHPANFCIFIRG 360
DB 301 LFEHESHVTOAGVQWPNLGSLOPLPGLKRFSCSLPSSWDYGHLPHPANFCIFIRG 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375

RESULT 3

US-09-964-667-2
Sequence 2, Application US/09964667
Publication No. US20030033621A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
Wands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Preventio
of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,667

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609,4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-964-667-2

Query Match 100.0%; Score 2034; DB 12; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLPRLCEGNGAISAHRNRLPGSSDPSASASPVAGITGMCTHARLILYFFLEVEMF 60
DB 1 MEFSLLPRLCEGNGAISAHRNRLPGSSDPSASASPVAGITGMCTHARLILYFFLEVEMF 60
QY 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120
DB 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120
QY 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
DB 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
DB 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
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DB 301 LFMESHVYTOAGVQWRNLSLOPLPPGKRRSCSLSPSSMDYGHLPHPANFCIFIRG 360
QY 361 VSPYLSGMSQTPDLR 375
DB 361 VSPYLSGMSQTPDLR 375

RESULT 4
US-09-872-968-2
Sequence 2, Application US/09872968
Publication No. US20030050262A1
GENERAL INFORMATION:
APPLICANT: Wands, Jack R
APPLICANT: de la Monte, Suzanne M
TITLE OF INVENTION: Inhibition of Neurodegeneration
FILE REFERENCE: 21486-047
CURRENT APPLICATION NUMBER: US/09/872,968
CURRENT FILING DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-09-872-968-2

Query Match 100.0%; Score 2034; DB 12; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120
DB 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120

QY 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
DB 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
DB 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
QY 301 LFMESHVYTOAGVQWRNLSLOPLPPGKRRSCSLSPSSMDYGHLPHPANFCIFIRG 360
DB 301 LFMESHVYTOAGVQWRNLSLOPLPPGKRRSCSLSPSSMDYGHLPHPANFCIFIRG 360
QY 361 VSPYLSGMSQTPDLR 375
DB 361 VSPYLSGMSQTPDLR 375

RESULT 5
US-10-146-130-2
Sequence 2, Application US/10146130
Publication No. US20030004107A1
GENERAL INFORMATION:
APPLICANT: AVERBACK, PAUL
TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
FILE REFERENCE: 59003.000007
CURRENT APPLICATION NUMBER: US/10/146,130
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
US-10-146-130-2

Query Match 100.0%; Score 2034; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MEFSLLPRLCEGNGAISAHRNRLPGSSDPSASASPVAGITGMCTHARLILYFFLEVEMF 60
QY 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120
DB 61 LHVGAAGLELPTSDPSVASASOSARYRTGHHARLCLANFCGRNRVSLMCPSPSPELKOST 120
QY 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
DB 121 CUSLPKCMYRRAAAYPGLEFLFELRHRCPTLTODEVQWCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
DB 181 VAGTDMHHYTWLIFIFINFLROSINSYTOAGVQWRNLSLOPLPPGFKLSPCLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
QY 301 LFMESHVYTOAGVQWRNLSLOPLPPGKRRSCSLSPSSMDYGHLPHPANFCIFIRG 360
DB 301 LFMESHVYTOAGVQWRNLSLOPLPPGKRRSCSLSPSSMDYGHLPHPANFCIFIRG 360
QY 361 VSPYLSGMSQTPDLR 375
DB 361 VSPYLSGMSQTPDLR 375

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RESULT 6
US-10-092-934-10
; Sequence 10, Application US/10092934
; Publication No. US20030054990A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHODS OF USING NEURAL THREAD PROTEINS TO TREAT TUMORS
; TITLE OF INVENTION: AND CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018792-0199
; CURRENT APPLICATION NUMBER: US/10/092,934
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/273,957
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-934-10
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Query Match      100.0%; Score 2034; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MERSLLPRLCNGAISAHRNRLPGSSDPSASAPVAGITGCTHARLLIYFVLVEEF 60
QY 61 LHVGAGLELPTSDPSVASASQARYRGHARCLANFCGRNVSLMCPMSPELKOST 120
Db 61 LHVGAGLELPTSDPSVASASQARYRGHARCLANFCGRNVSLMCPMSPELKOST 120
QY 121 CLSLPKCWDYRAAVPGFLIFELRHRCPTLTQDEVOMCHSSLOPSTPEIKHPASASQ 180
Db 121 CLSLPKCWDYRAAVPGFLIFELRHRCPTLTQDEVOMCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTDMHHTWLIFFIFENFLRQSLNSVTQAGVQWNLGSLQPLPGFKLFSCPSLSS 240
Db 181 VAGTDMHHTWLIFFIFENFLRQSLNSVTQAGVQWNLGSLQPLPGFKLFSCPSLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIENFC 300
Db 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIENFC 300
QY 301 LFEMESHVTOAGVQWPNLGLQPLPGIKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Db 301 LFEMESHVTOAGVQWPNLGLQPLPGIKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGMSQTPDLR 375
Db 361 VSPYLSGMSQTPDLR 375
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RESULT 7
US-10-153-334-1
; Sequence 1, Application US/10153334
; Publication No. US20030096350A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000006
; CURRENT APPLICATION NUMBER: US/10/153,334
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 60/293,156
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-334-1
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Query Match      100.0%; Score 2034; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MERSLLPRLCNGAISAHRNRLPGSSDPSASAPVAGITGCTHARLLIYFVLVEEF 60
Db 1 MERSLLPRLCNGAISAHRNRLPGSSDPSASAPVAGITGCTHARLLIYFVLVEEF 60
QY 61 LHVGAGLELPTSDPSVASASQARYRGHARCLANFCGRNVSLMCPMSPELKOST 120
Db 61 LHVGAGLELPTSDPSVASASQARYRGHARCLANFCGRNVSLMCPMSPELKOST 120
QY 121 CLSLPKCWDYRAAVPGFLIFELRHRCPTLTQDEVOMCHSSLOPSTPEIKHPASASQ 180
Db 121 CLSLPKCWDYRAAVPGFLIFELRHRCPTLTQDEVOMCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTDMHHTWLIFFIFENFLRQSLNSVTQAGVQWNLGSLQPLPGFKLFSCPSLSS 240
Db 181 VAGTDMHHTWLIFFIFENFLRQSLNSVTQAGVQWNLGSLQPLPGFKLFSCPSLSS 240
QY 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIENFC 300
Db 241 WDYRRPRLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIENFC 300
QY 301 LFEMESHVTOAGVQWPNLGLQPLPGIKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
Db 301 LFEMESHVTOAGVQWPNLGLQPLPGIKRFSCSLSPSSWDYGHLPHPANFCIFIRGG 360
QY 361 VSPYLSGMSQTPDLR 375
Db 361 VSPYLSGMSQTPDLR 375
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RESULT 8
US-10-198-069-1
; Sequence 1, Application US/10198069
; Publication No. US20030096756A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003-000009
; CURRENT APPLICATION NUMBER: US/10/198,069
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-069-1
```

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Query Match      100.0%; Score 2034; DB 15; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MERSLLPRLCNGAISAHRNRLPGSSDPSASAPVAGITGCTHARLLIYFVLVEEF 60
Db 1 MERSLLPRLCNGAISAHRNRLPGSSDPSASAPVAGITGCTHARLLIYFVLVEEF 60
QY 61 LHVGAGLELPTSDPSVASASQARYRGHARCLANFCGRNVSLMCPMSPELKOST 120
```



```
Db      61 LHVGOAGLELPTSDPSVASASARYRTGHNARLCLANCGNRNRYSLMCPSPBELKOST 120
        |||
Qy      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Db      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Qy      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Db      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Qy      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Db      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Qy      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
Db      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
Qy      361 VSPYLSGWSQTPDLR 375
        |||
Db      361 VSPYLSGWSQTPDLR 375
        |||
```

```
RESULT 9
US-10-157-031-299
; Sequence 299, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krakovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; -CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 299
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-299
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Query Match      100.0%, Score 2034, DB 15, Length 375;
Best Local Similarity 100.0%, Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 MEFSLLRLPRLCNGAISAHRNRLRPGSSDPSASAPVAGITGMCTHARLILFVLEMEF 60
        |||
Db      1 MEFSLLRLPRLCNGAISAHRNRLRPGSSDPSASAPVAGITGMCTHARLILFVLEMEF 60
        |||
Qy      61 LHVGOAGLELPTSDPSVASASARYRTGHNARLCLANCGNRNRYSLMCPSPBELKOST 120
        |||
Db      61 LHVGOAGLELPTSDPSVASASARYRTGHNARLCLANCGNRNRYSLMCPSPBELKOST 120
        |||
Qy      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Db      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Qy      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Db      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Qy      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Db      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Qy      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
Db      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
```

```
Qy      361 VSPYLSGWSQTPDLR 375
        |||
Db      361 VSPYLSGWSQTPDLR 375
        |||
```

```
RESULT 10
US-10-198-070-1
; Sequence 1, Application US/10198070
; Publication No. US20030109437A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; APPLICANT: GEMMELL, JACK
; TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
; CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 59003.000008
; CURRENT APPLICATION NUMBER: US/10/198,070
; -CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,161
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/306,150
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/331,477
; PRIOR FILING DATE: 2001-11-16
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-070-1
```

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Query Match      100.0%, Score 2034, DB 15, Length 375;
Best Local Similarity 100.0%, Pred. No. 3.9e-184;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 MEFSLLRLPRLCNGAISAHRNRLRPGSSDPSASAPVAGITGMCTHARLILFVLEMEF 60
        |||
Db      1 MEFSLLRLPRLCNGAISAHRNRLRPGSSDPSASAPVAGITGMCTHARLILFVLEMEF 60
        |||
Qy      61 LHVGOAGLELPTSDPSVASASARYRTGHNARLCLANCGNRNRYSLMCPSPBELKOST 120
        |||
Db      61 LHVGOAGLELPTSDPSVASASARYRTGHNARLCLANCGNRNRYSLMCPSPBELKOST 120
        |||
Qy      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Db      121 CUSLPKCDYRRAAVPGLFLEFLHRCPTLTODEVOWCDHSSLOPSTPEIKHPPASASQ 180
        |||
Qy      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Db      181 VAGTDMHHYTWLIFIFNPLROSLNSTOAGVOWRNIGSLQPLPFGFKLSCPSLSS 240
        |||
Qy      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Db      241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
        |||
Qy      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
Db      301 LFEEMESHVTOAGVOWPNIGSLQPLPGLKRFSCSLSPSSWDYGHLPHPANFCIFIRG 360
        |||
Qy      361 VSPYLSGWSQTPDLR 375
        |||
Db      361 VSPYLSGWSQTPDLR 375
        |||
```

```
RESULT 11
US-09-995-494-107
; Sequence 107, Application US/09995494
; Patent No. US20020127578A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
```

APPLICANT: Recipon, Herve
APPLICANT: Cafferey, Robert
APPLICANT: Ali, Shujath
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Chen, Sei-yu
TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0293
CURRENT APPLICATION NUMBER: US/09/995,494
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,176
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 107
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapien
US-09-995-494-107

Query Match 36.1%; Score 734.5; DB 11; Length 361;
Best Local Similarity 43.1%; Pred. No. 38-61; Indels 127; Gaps 12;
Matches 185; Conservative 24; Mismatches 93;

QY 6 LLPLRCNGAISAHNRLPGSSDSPASAPVAGITGM-----CTHARL----- 49
DB 1 LLPLRCGSGTMAHCRKLKLGSDLPASASRYGCTGKRQPTMGCTSCAHQIGLFPVAN 60
QY 50 -----ILYFLVEMEFLLVAGAGLEPLTSDPSVASASARYRGTGHARLCLIA 97
DB 61 FERSFYILGTSPLLDLMLIMTF-----FALLIHVLF- 94
QY 98 NEFCNRYSLMCP--SMSPELKOSTCLSLPKCMWRRAVPGFLTFLRHC----- 148
DB 95 -----NRSLCCPGASLTLGLFAFACLSLPRKMDTYTGPL-LPLDIFLYOCCLSFYELN 148
QY 149 PTLTDEVQWCDHSLQSTPEIKHPASASQVAGTKDMHAYTWLIFIEFELRQSLNS 208
DB 149 TVFOHAEV-----LIFQWMPYLLRWSLHS 172
QY 209 VTAQVQWRNIGSLQPLPPGFKLFGSPCLSSMDYRR--PRLAN--FVFLVEMGFTWFA 265
DB 173 VAQAGVQWNCIGSLQPLPRFRFSCSLSSWMDHRAHPCLANLFPFLVDQSFMTLA 232
QY 266 RLILISGPC-DLPASASQASAGITGVSH-----HARLIENCLFEMES 306
DB 233 RLVLNARSQGLPARPASQASAGITGVRHCHWPKSEKFAADSHIGLAHFAFEFFEFPAVAS 292
QY 307 HSYTQAGVQWPNLGLQPLPGCLKRFSCLSLPSWDYGLPHPHANFCIFITRGVSPYLS 366
DB 293 HPIAAGVQWRDLGSLQPPPGFKQFLCLSLPSWDYRRAPRANFCIFSRDGVSPCWT 352
QY 367 GMSOTPDLR 375
DB 353 GMSOTPDLR 361

RESULT 12
US-10-007-280A-140
Sequence 140, Application US/10007280A
Publication No. US20030059784A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
APPLICANT: Salceda, Susana
APPLICANT: Chenghua, Liu
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Pro
FILE REFERENCE: DEX-0257
CURRENT APPLICATION NUMBER: US/10/007,280A
CURRENT FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/246,640
PRIOR FILING DATE: 2000-11-08
NUMBER OF SEQ ID NOS: 238

SOFTWARE: PatentIn version 3.1
SEQ ID NO: 140
LENGTH: 449
TYPE: PRT
ORGANISM: Homo sapien
US-10-007-280A-140

Query Match 35.8%; Score 729; DB 15; Length 449;
Best Local Similarity 42.6%; Pred. No. 1.38-60;
Matches 196; Conservative 40; Mismatches 122; Indels 102; Gaps 19;

QY 6 LLPLRCNGAISAHNRLPGSSDSPASAPVAGITGMCTHARL-----ILYFLVE 57
DB 1 LLPLRCGSGTMAHCRKLKLGSDLPASASRYGCTGKRQPTMGCTSCAHQIGLFPVAN 60
QY 58 MEFLVAGAGLEPLTSDPSVASASARYRGTGHARL-----LANFC--- 100
DB 61 MRFHYVQAGLELLSSDPPISASQAGITGISH---CTWPMHDSFISGAEPLTFAYTW 117
QY 101 -GRNRSL-----MCPMSPELKOSTCLSLPKCMWRRAVPGFLTFLRHC-----F 139
DB 118 PGRKPIPLTLLILYBPGDVLVAFRTELYASPSRQOPASDTARESMGNCNAVPPFLKRW 177
QY 140 ILFLRHRCPPLTQDEV-----QWCD--HSLQSTPEIKHPA-----SASQVAGTKD 186
DB 178 LIF-----CPFSNOSHMTTKSKMAEVPHPRRALPAMKQKAKANENSGSVTEPSSSAS 232
QY 187 MHHTWLFIFIFN-----ELRQSLNSVTAQVQW---RNGSLQPLPPGFKLFGSPCLLS 239
DB 233 ILHARMDV-PLINALIYFLRQSLNSVAQAGVQWCGADLSLQPLPPGFAFPCLSLLS 291
QY 240 SMDYRR--PRLANFEVFLVEMGFTWFAHRLISGFCDLPASASQASAGITGVSHAR---- 294
DB 292 SMDYRSLPPCANFVFLVETLGHFHSQ--ISASAPCDPASASQASAGITGSHCAQPDVY 350
QY 295 -----LIENFCLEFEMESHSYTAQVQWPNLG-----SLQPLPPGLKRSC 334
DB 351 YVSGYIGKODRCYLFEEFFEFETESRTVAQAG--RLERSQISTRRSLQPLPPGLKRSC 409
QY 335 LSLPSMDYGLPHPHANFCIFITRGVSPYLSGMSOTPD 374
DB 410 LSLSSMDYRCPPRLAHFCTFSRDGVSPCWSGMSLSD 449

RESULT 13
US-09-989-920-245
Sequence 245, Application US/09989920
Patent No. US20020172957A1
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 245
LENGTH: 183
TYPE: PRT
ORGANISM: Homo sapien
US-09-989-920-245

Query Match 21.1%; Score 428.5; DB 11; Length 183;
Best Local Similarity 57.0%; Pred. No. 1.1e-32;
Matches 102; Conservative 13; Mismatches 51; Indels 13; Gaps 7;

QY 209 VTAQVQWRNIGSLQPLPPGFR-LFS--CPSLSSWDRRPPRLANF--FVFLVEMGFT- 262

Db 1 LTPACVPMCHLGSLOPLPPRFKAVFSRLASLEVAMDRAPSHARLISLAFVETGFSB 60
QY 263 MFAHILILSGPDDL-PASASOSAGITGVSHH--ARLIEN---FCLFEMESHVYQAGVQ 315
Db 61 TVARLVSNMWPVPPPLPSOSAGITGVGPPLCLARPLPPHPPFFFFDMEASHATQAGVQ 120
QY 316 WPNLGSLOPLPGLRFSCLSLPSSMDYGHLPHPANFCIFIRGCVSPYLSGMSQTPDL 374
Db 121 WRHLGSLQPPPPMFKASSCLSLSSMDYRRPPPRRAICIFSRDGVSRCAPGMSRSPDL 179

RESULT 14

US-10-157-031-291
Sequence 291, Application US/10157031
Publication No. US20030108890A1
GENERAL INFORMATION:
APPLICANT: Batanova, A. V.
APPLICANT: Yankovsky, N. K.
APPLICANT: Kozlov, A. P.
APPLICANT: Lobashev, A. V.
APPLICANT: Krukovskaya, L. L.
TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
FILE REFERENCE: 2760-103
CURRENT APPLICATION NUMBER: US/10/157,031
PRIORITY FILING DATE: 2002-05-30
NUMBER OF SEQ ID NOS: 415
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 291
LENGTH: 673
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(673)
OTHER INFORMATION: X = unknown
US-10-157-031-291

Query Match 18.8% Score 382.5; DB 15; Length 673;
Best Local Similarity 33.2%; Pred. No. 1.3e-27;

Matches 128; Conservative 19; Mismatches 111; Indels 127; Gaps 17;

QY 16 ISAHNRLRPGSSSDSPASAPVAGITGMCTHARLLLYFLVEMEFLLHVGAGLELPTSD 75
Db 371 VLHGSLLNLGSSDSPASVSRVAGITGMGRHMLI-YVFLIETQFHNDQAGLKLITSD 429
QY 76 PSVSASQSRARYTGTHARLCLANFCGRNVSLMCPMSPE-LKOSTCJSLPKCMDYRRAA 134
Db 430 -----LPSWSPKVLGXQAXATTPSXXXF---V 453
QY 135 VPGFLIFLFL-----RHRCP---TLTQDEVQWCHSSLOPSTPEIKHPPASA 178
Db 454 FGGFFFFFALEFLRLXALALTPRLCCSGKFWLTAASTSW-QAILLPLSPVXLGLQAWA 512
QY 179 SOVAGT---KDMHYTWLIFIFINFLROSLSVYQAGVQWRNLGSLQPLPPGFKLFSC 234
Db 513 A-IPGKFMFXRHSFTMLI-----RLVSNKAPV-----ICPPG----- 546
QY 235 PSLSSMDYRR-PPRLANFEVFLVEMGFTMFARLLISGCDLPASASOSAGITGVSHHA 293
Db 547 LPRKCMDDRRPPHAPAXXLFL---GVFFF----- 572
QY 294 RLIFNFCLEFEMESHVYQAGVQ---PNLGSLOPLPGLKRSCSLSSMDYGHLPHP 350
Db 573 --FLLCFCFXDRPLLXHPG--WSAVASFGSLQPPGFKRSCCLPCSDYRHGPPFL 628
QY 351 ANFCIFIRGCVSPYLSGMSQTPDLR 375
Db 629 ANLCIFNRDVTYSPCXSGMSQTPDLK 653

RESULT 15
US-10-078-090-143

Sequence 143, Application US/10078090
Publication No. US20030044815A1
GENERAL INFORMATION:

APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Hu, Ping
APPLICANT: Recipon, Herve
APPLICANT: Karra, Kalpana
APPLICANT: Caferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
FILE REFERENCE: DEX-0312
CURRENT APPLICATION NUMBER: US/10/078,090
PRIORITY FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/268,999
PRIORITY FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 210
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 143
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapien
US-10-078-090-143

Query Match 16.3% Score 332; DB 15; Length 108;
Best Local Similarity 67.6%; Pred. No. 7.5e-24;

Matches 73; Conservative 7; Mismatches 26; Indels 2; Gaps 2;

QY 201 FLROSLSVYQAGVQWRNLGSLQPLPPGFKLFSCPSLSSMDYRR-PPRLANFEVFLVEM 259
Db 1 FLROSLSVYQAGVQWRNLGSLQPLSLRKFASCLSLSSMDYRRHAPHPHAFVFLVEM 60
QY 260 GFTMFARLLISGCDLPASASOSAGITGVSHHARLI-FNCLFEMES 306
Db 61 GFTVLARWVSISATHDPPALACOSAGITGARHPRLIHIFLIFEYOS 106

Search completed: July 17, 2003, 18:29:00
Job time : 56 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 18:13:08 ; Search time 81 Seconds
(without alignments)
953.922 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MEFSLLPRLECGAISAHR.....FIRGVSPLYSGMSQPDLR 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2034	100.0	375	4	060448	G60448 homo sapien
2	316	15.5	152	4	09NX85	G9NX85 homo sapien
3	273.5	13.4	118	4	09H387	G9H387 homo sapien
4	263.5	13.0	73	4	096AN9	G96AN9 homo sapien
5	262	12.9	118	4	09P195	G9P195 homo sapien
6	261	12.8	66	4	096HL9	G96HL9 homo sapien
7	259	12.7	232	4	09H5R3	G9H5R3 homo sapien
8	257	12.6	162	4	09H5D5	G9H5D5 homo sapien
9	255	12.5	72	4	08TB48	G8TB48 homo sapien
10	254.5	12.5	239	4	09NX17	G9NX17 homo sapien
11	253	12.4	171	4	09H728	G9H728 homo sapien
12	252.5	12.4	666	4	P78525	F78525 homo sapien
13	250	12.3	238	4	08WT23	G8WT23 homo sapien
14	248	12.2	151	4	09HA67	G9HA67 homo sapien
15	247.5	12.2	130	4	09HBS7	G9HBS7 homo sapien
16	247	12.1	84	4	09UHT1	G9UHT1 homo sapien

17	246.5	12.1	162	4	09BYA5	G9BYA5 homo sapien
18	237.5	11.7	169	4	09H397	G9H397 homo sapien
19	232.5	11.4	208	4	09NW14	G9NW14 homo sapien
20	231.5	11.4	96	6	09BGU8	G9BGU8 macaca fasc
21	228.5	11.2	350	4	096NA4	G96NA4 homo sapien
22	227	11.2	122	6	09BOW3	G9BOW3 macaca fasc
23	226.5	11.1	687	4	09NXX7	G9NXX7 homo sapien
24	225	11.1	83	4	096ID7	G96ID7 homo sapien
25	225	11.1	165	4	096LS9	G96LS9 homo sapien
26	224.5	11.0	396	4	09UL10	G9UL10 homo sapien
27	223.5	11.0	127	4	09H743	G9H743 homo sapien
28	221.5	10.9	179	4	096MD7	G96MD7 homo sapien
29	221	10.9	163	4	096MM0	G96MM0 homo sapien
30	214.5	10.5	90	4	096IG1	G96IG1 homo sapien
31	213	10.5	102	4	09P147	G9P147 homo sapien
32	212	10.4	135	6	095KE1	G95KE1 macaca fasc
33	211	10.4	62	4	096FS0	G96FS0 homo sapien
34	208.5	10.3	54	4	08WUD5	G8WUD5 homo sapien
35	208.5	10.3	67	4	08TCD4	G8TCD4 homo sapien
36	208.5	10.3	231	4	09NR08	G9NR08 homo sapien
37	205.5	10.1	139	4	09BVD9	G9BVD9 homo sapien
38	203.5	10.0	111	4	09H3C0	G9H3C0 homo sapien
39	203.5	10.0	120	4	09H6G8	G9H6G8 homo sapien
40	203	10.0	109	4	08W239	G8W239 homo sapien
41	202	9.9	133	4	096JRS	G96JRS homo sapien
42	199.5	9.8	61	4	09UI48	G9UI48 homo sapien
43	199	9.8	61	4	09BRC4	G9BRC4 homo sapien
44	198	9.7	124	4	096MP3	G96MP3 homo sapien
45	194.5	9.6	126	4	09UHT2	G9UHT2 homo sapien

ALIGNMENTS

RESULT 1

ID 060448 PRELIMINARY; PRT: 375 AA.

AC 060448;

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-ANG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Neuronal thread protein AD7c-NTP.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=NEURONAL;

RA de la Monte S.M., Ghanbari K., Frey W., Beheshlt I., Hauser S.A.,

RA Ghanbari H.A., Wands J.R.;

RT "Characterization of the AD7c-NTP cDNA and its expression in the brain

RT and cerebrospinal fluid of patients with Alzheimer's disease.";

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF010144; AAC08737.1; -

SQ SEQUENCE 375 AA; 41720 MW; 955443950A5BFEPD CRC64;

Query Match 100.0%; Score 2034; DB 4; Length 375;

Best Local Similarity 100.0%; Pred. No. 2.2e-199;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFSLLPRLECGAISAHRNLRLPGSSDSPASASPVAGITGCTHARILYFFLVEMEF 60

DB 1 MEFSLLPRLECGAISAHRNLRLPGSSDSPASASPVAGITGCTHARILYFFLVEMEF 60

QY 61 LHYGAGLELPSPDPSVSASOSARYRTGHHARLCLANFCGRNRVSLMCPMSPELKOST 120

DB 61 LHYGAGLELPSPDPSVSASOSARYRTGHHARLCLANFCGRNRVSLMCPMSPELKOST 120

QY 121 CUSLPKCMYRRAVAGLFLFLRHRCPITLQDEVQWCHSSLOSTPEIKHPPASASO 180

DB 121 CUSLPKCMYRRAVAGLFLFLRHRCPITLQDEVQWCHSSLOSTPEIKHPPASASO 180

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OY 181 VAGTKDMHYTWLFIETFIENFLRQSLNSTOAGVQWRNIGSLQPLPGKFLSPCLSS 240
DB 181 VAGTKDMHYTWLFIETFIENFLRQSLNSTOAGVQWRNIGSLQPLPGKFLSPCLSS 240
OY 241 WDYRRPRLANFEVLVEGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
DB 241 WDYRRPRLANFEVLVEGFTMFARLLISGPCDLPASASOSAGITGVSHHARLIFNFC 300
OY 301 LFEEMESHSTOAGVQWRNIGSLQPLPGKFLSPCLSSMDYGHLPHPANFCIFIRNG 360
DB 301 LFEEMESHSTOAGVQWRNIGSLQPLPGKFLSPCLSSMDYGHLPHPANFCIFIRNG 360
OY 361 VSPYLSGMSQTPDLR 375
DB 361 VSPYLSGMSQTPDLR 375

RESULT 2
O9NX85 PRELIMINARY: PRT: 152 AA.
ID 09NX85
AC 09NX85:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KAI0536 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohbayashi M., Nishii T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isono T., Sugano S.,
RT "NEO human cDNA sequencing project."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK000385; BAA91131.1;
SQ SEQUENCE 152 AA; 16568 MW; 59065F45AANA301B5 CRC64;

Query Match
Best Local Similarity 51.3%; Score 316; DB 4; Length 152;
Matches 80; Conservative 12; Mismatches 38; Indels 26; Gaps 6;

OY 173 HPP-----ASASQVAGTKDMHYTWLFIETFIENFLRQSLNSTOAGVQWRNIGSLQPLPG 228
DB 3 HSPRLVANPSQV-----LFELSLPEFF-FLRQSLVANAGVQWRNIGSLQPLPG 53
OY 229 FKLEFCPSLSSMDYRRPRLANFEVLVEGFTMFARL---ILISGPCDLPASASOSAG 285
DB 54 FKQFCSLILSSMDYRRPRLANFEVLVEGFTMFARL---ILISGPCDLPASASOSAG 111
OY 286 ITGVSHHAR-----LIFNFCLEEMESHSTOAG 313
DB 112 ITGSGSHRQPTSSNPYGIIVFFLVPKTFSGMSQKAG 147

RESULT 3
O9H387 PRELIMINARY: PRT: 118 AA.
ID 09H387
AC 09H387:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE PRO2550.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zhang C., Yu Y., Zhang S., Wei H., Bi J., Zhou G., Dong C., Zai Y.,

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RA Xu W., Gao F., Liu M., He F.;
RT "Functional prediction of the coding sequences of 75 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF130089; AAC35515.1;
SQ SEQUENCE 118 AA; 13257 MW; 94688870CAC8760D CRC64;

Query Match
Best Local Similarity 63.1%; Score 273.5; DB 4; Length 118;
Matches 65; Conservative 4; Mismatches 27; Indels 7; Gaps 4;

OY 196 IFIENFLRQSLNSTOAGVQWRNIGSLQPLPGKFLSPCLSSMDYRR-PPRLANFEV 254
DB 4 IFIENFLRQSLNSTOAGVQWRNIGSLQPLPGKFLSPCLSSMDYRR-PPRLANFEV 62
OY 255 FLVEGFTMFARL---ILISGPCDLPASASOSAGITGVSHHAR 294
DB 63 FLVEGFTMFARL---ILISGPCDLPASASOSAGITGVSHHAR 103

RESULT 4
O96AN9 PRELIMINARY: PRT: 73 AA.
ID 096AN9
AC 096AN9:
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Similar to hypothetical protein PRO1722.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016905; AAH16905.1;
KW Hypothetical protein.
SQ SEQUENCE 73 AA; 8348 MW; 673F61B85300AC2F CRC64;

Query Match
Best Local Similarity 13.0%; Score 263.5; DB 4; Length 73;
Matches 51; Conservative 5; Mismatches 16; Indels 1; Gaps 1;

OY 304 MESHSVQAGVQWRNIGSLQPLPGKFLSPCLSSMDYGHLPHPAN-FCIFIRGVS 362
DB 1 MESHSVQAGVQWRNIGSLQPLPGKFLSPCLSSMDYGHLPHPAN-FCIFIRGVS 60
OY 363 PYLSGMSQTPDLR 375
DB 61 PCWPGMSQTPDLR 73

RESULT 5
O9P195 PRELIMINARY: PRT: 118 AA.
ID 09P195
AC 09P195:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE PRO1722.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhang Y., Zhou G., Bi J., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 79 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";

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[illegible]

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SO SEQUENCE 232 AA; 26703 MW; 56946BE74C226FF5 CRC64;

Query Match 12.7%; Score 259; DB 4; Length 232;
Best Local Similarity 67.6%; Pred. No. 2.7e-18;
Matches 50; Conservative 5; Mismatches 19; Indels 0; Gaps 0

QY 302 FEMESHVATQAGVOMPNLGSLOPLRPGLKRFSCSLSPSMDYGHLPHPANCFIPIRGV 361
DB 159 MWTQSRVATQAGVOMCDCLLOPPSPRRKRFSCSLSPSMDIRHPPLANCFISRDGV 218
QY 362 SPYLGSWSQTPDLR 375
DB 219 SPCWPGWMSRTCDLR 232

RESULT 8
Q9H5D5 PRELIMINARY; PRT; 162 AA.
AC Q9H5D5;
DT 01-MAR-2001 (TREMBlrel. 16; Created)
DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19; Last annotation update)
DE CDNA: FLJ23555 fis, clone LNC09438.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Strausberg R.;

SEQUENCE 162 AA; 17632 MW; C9A857907E44D2E8 CRC64;

Query Match 12.6%; Score 257; DB 4; Length 162;
Best Local Similarity 47.0%; Pred. No. 2.8e-18;
Matches 63; Conservative 2; Mismatches 23; Indels 46; Gaps 2

QY 208 SVTQAGVOMNLGSLQPLRPGLKRFSCSLSPSMDYR-RPRLANFVFLVEMGFTMAR 266
DB 63 SVPRAGVQMCNLGSLQPLRPGLKRFKQFSLSPSSMGYSVAPPCPANNFFP----- 111
QY 267 LILISGPDRLPASASQSGAGITGVSHNHLIFLFCLEFEMESHVATQAGVOMPNLGSLOPL 326
DB 112 -----FEMESCSVPNAGVOMHDLGSQQPP 137

RESULT 9
Q8TB48 PRELIMINARY; PRT; 72 AA.
AC Q8TB48;
DT 01-JUN-2002 (TREMBlrel. 21; Created)
DT 01-JUN-2002 (TREMBlrel. 21; Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21; Last annotation update)
DE Similar to PR02550.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Strausberg R.;

```

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC024651; AA024651.1; -
 SO SEQUENCE 72 AA; 8162 MW; C1AF28BD98E2C1F0 CRC64;

Query Match 12.5%; Score 255; DB 4; Length 72;
 Best Local Similarity 66.7%; Pred. No. 1,7e-18;
 Matches 48; Conservative 5; Mismatches 19; Indels 0; Gaps 0;

QY 304 MESHVYQAGVQVMPNLTSLQPLPPGKRFSCSLSPSSMDYGHLPHPANCFITRGVSF 363
 DB 1 MESHICQAGVQVQVHHGLLOPPPPGKRFSCSLSPGWTGRPLPHANCFIENRHEVSP 60
 QY 364 YLGSWQTPDLR 375
 DB 61 CWPQCSRTPLDK 72

RESULT 10

Q9NX17 PRELIMINARY; PRT; 239 AA.

AC Q9NX17; 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE CDNA FLJ20489 fis, clone KAT08285.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Matarabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Oka T.,
 RA Suzuki Y., Ohtsuka M., Nishi T., Shibahara T., Tanaka T.,
 RA Nakamura Y., Isigai T., Sugano S.;
 RT "NEDD human cDNA sequencing project."
 SO Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK000496; BAA91205.1; -
 SO SEQUENCE 239 AA; 25728 MW; 5272FFA2C34214A5 CRC64;

Query Match 12.5%; Score 254.5; DB 4; Length 239;
 Best Local Similarity 64.2%; Pred. No. 8e-18;
 Matches 61; Conservative 6; Mismatches 25; Indels 3; Gaps 3;

QY 1 MEESLL-PRLENCATSAHNRRLPGSSDPSASPAVAGTGMCTHARLIFYFLVEME 59
 DB 120 LKMSLLSPRLSCSSAISHCHLRLPGSSNSPALASQVAGITGICHARQI-FEFLVETG 178
 QY 60 FLHVGQAGLEPTSDPSVSASQAR-YRTGHHAR 93
 DB 179 FCHVGQAGLELLISGDSFASAFQSGITGVSHRAR 213

RESULT 11

Q9H728 PRELIMINARY; PRT; 171 AA.

AC Q9H728; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DE 01-MAR-2001 (Tremblrel. 16, last annotation update)
 DE CDNA: FLJ21463 fis, clone COL04765.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawabata A., Hiki T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isigai T., Sugano S.;
 RT "NEO human cDNA sequencing project."
 SO Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK025116; BAB15071.1; -

SO SEQUENCE 171 AA; 18436 MW; DDC546D275038FAF CRC64;

Query Match 12.4%; Score 253; DB 4; Length 171;
 Best Local Similarity 69.3%; Pred. No. 7.7e-18;
 Matches 61; Conservative 3; Mismatches 20; Indels 4; Gaps 3;

QY 6 LPLENCATSAHNRRLPGSSDPSASPAVAGTGMCTHARLIFYFLVEMFELVHQ 65
 DB 63 LSPRLCNCATSAHCHLRLPDSNSPASASQVAGITGSHHNAHLI-FEFLVETGCHVQ 121
 QY 66 AGLEPTSDPSVSASQARVETG--HH 91
 DB 122 DLELLITSDPPASASQARVETG--TGMSSH 148

RESULT 12

P78525 PRELIMINARY; PRT; 666 AA.

AC P78525; 01-MAY-1997 (Tremblrel. 03, Created)
 DT 01-MAY-1997 (Tremblrel. 03, last sequence update)
 DE 01-MAR-2002 (Tremblrel. 20, last annotation update)
 DE MYB proto-oncogene protein (C-MYB).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=LIVER, AND PLACENTA;
 RA Westin E.H., Gorse K.M.;
 RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 3 MYB-LIKE DOMAINS.
 CC -1- SUCCESSFUL LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: U22376; AAB49034.1; -
 DR EMBL: U22376; AAB49034.1; -
 DR HSP; P06876; IMBE.
 DR InterPro: IPR001005; Myb DNA-binding.
 DR Pfam: PF00249; myb DNA-binding; 3.
 DR SMART: SM00395; SANT; 3.
 DR PROSITE: PS00037; MYB_1; 3.
 DR PROSITE: PS00334; MYB_2; 3.
 DR PROSITE: PS00900; MYB_3; 3.
 KW Activator; DNA-binding; Nuclear protein; Proto-oncogene; Repeat;
 RN Transcription regulation.
 FT DNA_BIND 34 86 MYB.
 FT DNA_BIND 87 138 MYB.
 FT DNA_BIND 139 189 MYB.
 SO SEQUENCE 666 AA; 75525 MW; BF91C8F858EA12DF CRC64;

Query Match 12.4%; Score 252.5; DB 4; Length 666;
 Best Local Similarity 63.4%; Pred. No. 4.4e-17;
 Matches 59; Conservative 6; Mismatches 21; Indels 7; Gaps 4;

QY 213 GVCNRNIGSLQPLPPGKRFSCSLSPSSMDYR-PRLANFEFLVEMGFTEFARL---I 268
 DB 568 GVCNHDHGSLOPLPPGKRFSCSLSPSSMDYRPPPPRAN-FEFLVETGFLHVGQAGLE 626
 QY 269 LISGCDLPASASQARVETG--HH 91
 DB 627 LTSG--DLPASASQARVETG--HH 91

RESULT 13

Q8WT23 PRELIMINARY; PRT; 238 AA.

AC Q8WT23; 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
 DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Hypothetical 27.2 kDa protein.
 OS Homo sapiens (Human).
 DR EMBL: AK025116; BAB15071.1; -

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: July 17, 2003, 18:07:48 ; Search time 23 Seconds
(without alignments)
676.244 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLPRLCNCALSAHR.....FIRGVSPLYSGWQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112392

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	595	29.3	587	1	ALU2_HUMAN
2	568	27.9	587	1	ALU3_HUMAN
3	549.5	27.0	591	1	ALU8_HUMAN
4	498.5	24.5	591	1	ALU1_HUMAN
5	389	19.1	585	1	ALU5_HUMAN
6	357.5	17.6	593	1	ALU6_HUMAN
7	356.5	17.5	603	1	ALU4_HUMAN
8	330.5	16.2	593	1	ALU7_HUMAN
9	161	7.9	841	1	NEK4_HUMAN
10	101.5	5.0	438	1	SGCE_HUMAN
11	101	5.0	717	1	MTOL_HUMAN
12	100	4.9	629	1	2195_HUMAN
13	98.5	4.8	741	1	RED1_HUMAN
14	98	4.8	501	1	GRG2_HUMAN
15	96.5	4.7	1643	1	RRPO_NMV
16	91.5	4.5	631	1	HNF4_HUMAN
17	91.5	4.5	1776	1	POLR_OYMY
18	90.5	4.4	282	1	VMSA_MHYV6
19	90	4.4	431	1	VMSA_MHYV8
20	88	4.3	209	1	HS27_CANFA
21	88	4.3	726	1	ADDB_HUMAN
22	87	4.3	1153	1	NS2A_HUMAN
23	86.5	4.3	961	1	BASO_MOUSE
24	86.5	4.3	1886	1	GP21_RAT
25	85.5	4.2	832	1	DPOL_HPBVA
26	84	4.1	366	1	VMSA_HPBVA
27	84	4.1	843	1	DPOL_HPBVA
28	83.5	4.1	1304	1	S3B1_MOUSE
29	83	4.1	716	1	HGFL_MOUSE
30	83	4.1	763	1	DPOL_HPBVA
31	83	4.1	1216	1	AREP_RAT
32	82.5	4.1	481	1	DPOL_HPBVA
33	82.5	4.1	845	1	DPOL_HPBVA

34	82.5	4.1	1304	1	S3B1_HUMAN	075533 homo sapien
35	82	4.0	226	1	VMSA_HPBVA	P31869 hepatitis b
36	82	4.0	832	1	DPOL_HPBVA	P03156 hepatitis b
37	81.5	4.0	389	1	VMSA_HPBVA	P03138 hepatitis b
38	81.5	4.0	597	1	C4BP_HUMAN	P04003 homo sapien
39	81.5	4.0	843	1	DPOL_HPBVA	P17393 hepatitis b
40	81	4.0	723	1	TERM_ADECR	O96682 canine aden
41	81	4.0	901	1	Y298_HUMAN	O15016 homo sapien
42	80.5	4.0	389	1	VMSA_HPBVA	P12911 hepatitis b
43	80.5	4.0	413	1	GAT1_HUMAN	P15976 homo sapien
44	80.5	4.0	1299	1	JAK3_MOUSE	O62137 mus musculu
45	79.5	3.9	619	1	REL_HUMAN	O04864 homo sapien

ALIGNMENTS

RESULT 1
ID ALU2_HUMAN STANDARD: PRT: 587 AA.
AC P39189:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alu subfamily SB sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=95021758; PubMed=7935834;
RA Claverie J.-M., Makalowski W.,
RT "Alu alert.",
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RP MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.,
RT "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.",
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA "The Alu family developed through successive waves of fixation
Quentin Y.,
RT closely connected with primate lineage history.",
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Miosavljetic A.,
RT "Reconstruction and analysis of human Alu genes.",
RL J. Mol. Evol. 32:105-121(1991).
CC -I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
REPEATS.
CC -I- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC -I- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
ACID SEQUENCES.
CC -I- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
LIGATED WITH ALU-DERIVED SEQUENCE IN AN ORIENTATION. ALTHOUGH ALU
ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,

CC	CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC	OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC	CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC	DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC	THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC	BEING REPORTED.
CC	-1- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC	WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC	PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC	CODING NUCLEOTIDE SEQUENCE.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	entities requires a license agreement (See http://www.isb-slb.ch/announce/
CC	or send an email to license@isb-slb.ch).
CC	-----
CC	EMBL; U14568; -; NOT_ANNOTATED_CDS.
CC	Hypothetical protein.
FT	DOMAIN 1 FRAME-1.
FT	DOMAIN 100 194
FT	DOMAIN 198 292 FRAME-2.
FT	DOMAIN 296 391 FRAME-3.
FT	DOMAIN 395 489 FRAME-4.
FT	DOMAIN 493 587 FRAME-5.
FT	DOMAIN 587 63703 MM; 3EABAB3EB3929203 CNO64;
CC	-----
CC	SEQUENCE
CC	-----
CC	Query Match 29.3%; Score 595; DB 1; Length 587;
CC	Best Local Similarity 41.5%; Pred. No. 1,1e-45;
CC	Matches 153; Conservative 14; Mismatches 96; Indels 106; Gaps 8;
CC	-----
CC	6 LPLRLCNGAISAHNRNLRLPGSSDSPASASAPVAGITGCTAHRLILYFVLEMEFLHWGQ 65
CC	304 LSPRLCCGSAISACKRLPGSRHSPASASRVAGTGARHNRRLI-FVFLVETGFRHRYSQ 362
CC	66 AGLEPLTDDPSVASOSARVYRTGHNAHLCLANFCGRNRVSLMCPWSBELKQSTCLSLP 125
CC	363 DGLDILT-----SKSAR-----LGLP 378
CC	126 KCMWDYRAAVALGFLIEFLRRRCPTLTDQEWQCHDSSLQPSPEIKHPPASASQVACTK 185
CC	379 KCMQYRRPRPPAXXKFF-----XDGVSIC-----RQWASVARSRLTASAS-- 421
CC	186 DMNHYTWLILFIFINFLKQSLNSTYQAQVQWRNIGSLQDLPFGFLFECPSLTLSSMDVRR 245
CC	422 -----RVNAHLILPQPEXIGLOAPATTP----- 444
CC	246 PRLANFVFLVEMGFTMFARLLILSGCDLPPASASQAGITGVSHNRLLFTNCLFEME 305
CC	445 ---GXFLYFXRRGCFVLARWVISISXRPDRPPASASQSGAGITGVSHNRXXX---FFETE 497
CC	306 SHSYTQAQVQWRNIGSLQDLPFGFLKRESCLSLPSWSDYGHLPHPNANCIFIRGVASYPL 365
CC	498 SRSAVAQAVQWRNDLGSLOAPPGGFTFSCLSLPSWSDYRRPPRPNANCFIERSRDGVSPOX 557
CC	366 SGWSQTPDL 374
CC	558 PGWSRSPDL 566
CC	-----
CC	RESULT 2
CC	ALU3_HUMAN STANDARD; PRT; 587 AA.
CC	P39150; 01-FEB-1995 (Rel. 31, Created)
CC	01-FEB-1995 (Rel. 31, Last sequence update)
CC	16-OCT-2001 (Rel. 40, Last annotation update)
CC	Alu subfamily SBI sequence contamination warning entry.
CC	Homio sapiens (Human).
CC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

```

OX NCR1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021756; PubMed=7935934;
RA Claverie J.-M., Makalowski W.;
RN "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RN "Identifying coding exons by similarity search: alu-derived and other
potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RN "The Alu family developed through successive waves of fixation
closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J., Milosavljevic A.;
RN "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -I- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
REPEATS.
CC -I- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CODON, 'xxx' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC -I- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
ACID SEQUENCES.
CC -I- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES.
CC BEING REPORTED.
CC -I- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CODING NUCLEOTIDE SEQUENCE.
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U14569; -; NOT_ANNOTATED_CDS.
CC -----
KW Hypothetical protein
FT DOMAIN 1 96 FRAME-1.
FT DOMAIN 100 194 FRAME-2.
FT DOMAIN 198 292 FRAME-3.
FT DOMAIN 296 391 FRAME-4.
FT DOMAIN 395 489 FRAME-5.
FT DOMAIN 493 587 FRAME-6.
SQ SEQUENCE 587 AA: 63573 MW: 8504155720DEF235 CRC64;

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Query Match	27.9%;	Score 568;	DB 1;	Length 587;
Best Local Similarity	41.5%;	Pred. No. 2.9e-43;		
Matches 153; Conservative	15;	Mismatches 95;	Indels 106;	Gaps 10;

```

OY      6 LPLRELCNANSHNRRLRPGSSDDPASASPAAGTICMCTARLLVLFELWEMELHVG 65
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      304 LSRLLCCSGCISHNCKLRLPGSRHSPASASOVAAGTTGARHAYRL--TVFLVTEGFHFRSR 362
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      66 AGLELPTSDPASVASOSARVRYTGHHARLCLANFCGRNRVSLMCPMSPELOKOSTCLSP 125
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      363 DGLDLLT-----SXSNR-----LGLP 378
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      126 KCMYDRAAARPGILFELFLRNRCPTLTODEYQWCMCHSLDSTPEIKHNPASASQVATK 185
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      379 KCMYDRERPRRPAAXXFF-----XDGVSIC-----RPGMSA--VAGSR 414
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      186 DMHNYTWLFIFFNFRLQSLNSVYQAGVQMNINLSLOPLRPGFKLLSCPSLSSMRYR 245
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      415 -----LTAASSASRVHA-----ILLRPPKXLCIQAPRTTP----- 444
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      246 PRLANFVFLWEGFTMPARLILISCPDPLPASASOGATIGVSHARLTFNFCLEME 305
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      445 ----GXFLFXRXRGCTVLAGNVSTSXRRDPASPASOGATIGVSHARXXX---FEETE 497
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      306 SHSVTQAGVQMPNLSLOPLRPGLRFCSCLSLPSMWDYGHLPHPANFCIFIRGVSPLY 365
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      498 SRSVAQAGVQMRDLSIQARPPGTFPFSCLSLPSMWDYRRRLRPPANFCIPSRDGVSPFX 557
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY      366 SGMSTPDL 374
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      558 PGWSRSPDL 566
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 3

ALU8_HUMAN	STANDARD;	PRT;	591 AA.
ID AC	ALU8_HUMAN		
DT DT	P39195:		
DT DT	01-FEB-1995 (Rel. 31, Created)		
DT DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE DE	Alu subfamily SX sequence contamination warning entry.		
OS OS	Homo sapiens (Human).		
OC OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX OX	NCBI_TaxID=9606;		
RN RN	[1]		
RP RP	SEQUENCE FROM N.A.		
RX RX	MEDLINE=95021758; PubMed=7935834;		
RA RA	Claverie J.-M., Makalowski W.,		
RT RT	"Alu alert".		
RL RL	Nature 371:752-752(1994).		
RN RN	[2]		
RP RP	CONCEPT.		
RX RX	MEDLINE=92241891; PubMed=1572661;		
RA RA	Claverie J.-M.;		
RT RT	"identifying coding exons by similarity search: alu-derived and other		
RL RL	potentially misleading protein sequences.";		
RN RN	Genomics 12:838-841(1992).		
RN RN	[3]		
RP RP	ALU FAMILIES CLASSIFICATION.		
RX RX	MEDLINE=88333009; PubMed=91384422;		
RA RA	Ouentin Y.;		
RT RT	"The Alu family developed through successive waves of fixation		
RL RL	of closely connected with primate lineage history.";		
RN RN	J. Mol. Evol. 27:194-202(1988).		
RN RN	[4]		
RP RP	ALU FAMILIES CLASSIFICATION.		
RX RX	MEDLINE=91178815; PubMed=1706781;		
RA RA	Jurka J., Milosavljevic A.;		
RT RT	"Reconstruction and analysis of human Alu genes.";		
RL RL	J. Mol. Evol. 32:105-121(1991).		
CC CC	-1 MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE		

CC THAT ALU REPEATS FALL INTO 8 SUPERFAMILIES. THEREFORE, 8 ALU MARKING
CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC REPEATS.
CC
CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC
CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC ACID SEQUENCES.
CC
CC -1- CAUTION: ALU REBETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC ACTIVELY TRANSCRIBED BY POL. III. NORMAL TRANSCRIPTS MAY CONTAIN
CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC cDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED cDNAs
CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC BEING REPORTED.
CC
CC -1- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC CODING NUCLEOTIDE SEQUENCE.

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DR EMBL; U14574; -; NOT_ANNOTATED_CDS.

Accession	Protein	Length (aa)	PI	MW (kDa)	Gene
KW	Hypothetical protein	96			FRAME-1.
FT	DOMAIN	100	1.95		FRAME-2.
FT	DOMAIN	199	2.94		FRAME-3.
FT	DOMAIN	298	3.93		FRAME-4.
FT	DOMAIN	397	4.92		FRAME-5.
FT	DOMAIN	496	5.91		FRAME-6.
SO	SEQUENCE	591 AA;	64395 MW;		AC8154AD8A6BB280 CXC64;

Query Match	27.08%	Score 549.5	DB 1	Length 591
Best Local Similarity	38.98%	Pred. No. 1.3e-41		
Matches 150; Conservative	15;	Mismatches 84;	Indels 137;	Gaps 11;

Oy		6	LPLRLCNGAISAHNRNLPPGSSDSPASASPAGITGCTARLLVFEFLVMEFGLHVQ	65
Dd		306	LSPLRECGAISAHNLRPPGSSDSPASASAVAGITGARHNHARL-FEVLVEGTGHNVQ	364
Oy		66	AGLELPISDD--PSVSASQSARKYRTGHHARLCIANFCGRNRYSLMCSWS-----P	114
Dd		365	AGLELTISGDPRPVYLGLQAXATAPG----LRPXHXFFXDCDVSCLCPGMSAVARSRLTAT	420
Oy		115	ELKSTCSTLSPKCMD---YRRAVPGLFLFHLRHRCPTLTODEVOMCHSIQLSPTE	170
Dd		421	SASRQVALILPQPREDXLGLQARAATTGCXFLEFXKRGGFTMLAR-----LVSNSXPQ	471
Oy		171	IKHPPASQVAGATKDMHTWTLIFEFENFLRQSLNSVTQAGVQWRNLGSIQPLRPGEK	230
Dd		472	V-----IF-----	474
Oy		231	LFSCPLLSSWDYRR-PRPLANFEVLVEGMFTMARLLISGCDLPASASQSGAIGTV	289
Dd		475	-----LPKCMIDYRREPFR-----PASARXXX-----	495
Oy		290	SHARLILFNCLFEFESHSVTQAGVQWPNLGSLQPLPRGLKRFSCLSLPSSSWDYGHLRPH	349
Dd		496	-----FFETESRSVAQAGVQWMDLGSLQPLPRPGFGFRFSCLSLPSSSWDYRRARP	544

CC ACTIVELY TRANSCRIBED BY POL. III. NORMAL TRANSCRIPTS MAY CONTAIN
 CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
 CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CNAS
 CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
 CC ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
 CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
 CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
 CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
 CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
 CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
 CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
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 CC -----
 CC DR EMBL: U14572; NOT_ANNOTATED_CDS.
 CC KW Hypothetical protein.
 CC FT DOMAIN 1 97 FRAME-1.
 CC FT DOMAIN 101 196 FRAME-2.
 CC FT DOMAIN 200 295 FRAME-3.
 CC FT DOMAIN 299 395 FRAME-4.
 CC FT DOMAIN 399 494 FRAME-5.
 CC FT DOMAIN 498 593 FRAME-6.
 CC SQ SEQUENCE 593 AA: 64603 MW: 136EFP344AACD12A2 CRC64:
 CC
 CC Query Match 17.6%; Score 357.5; DB 1; Length 593;
 CC Best Local Similarity 48.2%; Pred. No. 2e-24;
 CC Matches 95; Conservative 6; Mismatches 47; Indels 49; Gaps 8;
 CC
 CC OY 4 SLLPRLCNGCAISHRRLRLPGSSDPSASPVAGTGMCHARTLIFYFLVEMEPHY 63
 CC DB 405 SLLPRLCNGCAISHRRLRLPGSSDPSASPVAGTGMCHARTLIFYFLVETGFLHV 463
 CC OY 64 GQAGLEPTSDPSVSASQASARYRTG--HHARLCIANFCGRNRYSLMCPMSW----- 113
 CC DB 464 GQAGLEPTSDPSVSASQASAGI--TGVSRRAR---XXXFFETEPSCCPGMSAMARSLT 519
 CC OY 114 -----PELKOSTCLSLPKCMYRRAAVGLTLPFLRHRCPTLTIDDEVQM 158
 CC DB 520 ATASARVQAILLPDPPEX-----LGLQAC-----ATTPGXFLYEXRGGFSLVR----- 564
 CC OY 159 CDHSLQSTPEIKHP 175
 CC DB 565 -----LVNSRQVIRPP 577
 CC
 CC RESULT 7
 CC ALU4_HUMAN
 CC ID ALU4_HUMAN STANDARD. PRT: 603 AA.
 CC AC P39191.
 CC DT 01-FEB-1995 (Rel. 31, Created)
 CC DT 01-FEB-1995 (Rel. 31, Last annotation update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE ALU subfamily SB2 sequence contamination warning entry.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CC OC NCBI_TaxID=9606;
 CC RN [1]
 CC RN SEQUENCE FROM N.A.
 CC RX MEDLINE=95021758; PubMed=7935834;
 CC RA Claverie J.-M.; Makalowski W.;
 CC "Alu alert.";

RL Nature 371:752-752(1994).
 RN [2]
 RN CONCEPT.
 RP MEDLINE=92241891; PubMed=1572661;
 RA Claverie J.-M.;
 RT "Identifying coding exons by similarity search: alu-derived and other
 RT potentially misleading protein sequences.";
 RT Genomics 12:838-841(1992).
 RN [3]
 RN ALU FAMILIES CLASSIFICATION.
 RP MEDLINE=88333009; PubMed=3138422;
 RA Quentin Y.;
 RT "The Alu family developed through successive waves of fixation
 RT closely connected with primate lineage history.";
 RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RN ALU FAMILIES CLASSIFICATION.
 RP MEDLINE=91178815; PubMed=1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
 CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
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 CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
 CC REPEATS.
 CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
 CC CODON. 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
 CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
 CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
 CC ACID SEQUENCES.
 CC -1- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
 CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
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 CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CNAS
 CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
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 CC -----
 CC DR EMBL: U14570; NOT_ANNOTATED_CDS.
 CC KW Hypothetical protein.
 CC FT DOMAIN 1 98 FRAME-1.
 CC FT DOMAIN 102 199 FRAME-2.
 CC FT DOMAIN 202 300 FRAME-3.
 CC FT DOMAIN 304 401 FRAME-4.
 CC FT DOMAIN 405 502 FRAME-5.
 CC FT DOMAIN 506 603 FRAME-6.
 CC SQ SEQUENCE 603 AA: 65272 MW: B8AADAD46BEA114 CRC64;
 CC
 CC Query Match 17.5%; Score 356.5; DB 1; Length 603;
 CC Best Local Similarity 30.3%; Pred. No. 2.5e-24;
 CC Matches 112; Conservative 28; Mismatches 115; Indels 115; Gaps 14;
 CC
 CC OY 76 PSVASOSARRYTGHHARLCIANFCGRNRYSLMCPMSWPELKOSTCLSLPKCMYRRAAV 135


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Db 156 PSYMGGRMAXTREAELAVSRDCA---TAVRSPAMATERDSVS-----KXKX 202
QY 136 PGLFLFLRHRG-PTLVDEVQMC-----DHSLQSTP-----KXKX 169
Db 203 PQA-----VAHACNSTLGRGGRGIMRSGDRDHPXQGETPSLTIKISRMRAPVVP 257
QY 170 -----EIKHP-----PASASOYAGTKDMHHYTLIFIFENFLR 203
Db 258 ATGEAEAEEMREPKRSIQXAEIAPLOSARVGRGSETPSKKXKF-----FLR 307
QY 204 QS--LNSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSMDYR--PPRLANFVFLVEMG 260
Db 308 RSLASPPRDCGLQWRNLGSLQAPLPDFTFSCSLSPSSMDYRPPRPPANFLYFXRRG 367
QY 261 FTFARLLISGPCDLPASASOSAGITGVSHHARLIFNF-----CLFEMES 306
Db 368 FTLLARMVSIKXPHDPASASOSAGITGVSHHARLIFNF-----CLFEMES 427
QY 307 HSVTQAGVQWRNLGSLQPLPPGKLFSCPSLLSMDYRPPRPPAN--FCIFIRGVSRY 364
Db 428 HCKLRF-----PCSRHSPPASASPVACTTG--AHRRALIFCIFSRRGVSPC 471
QY 365 LSGMSQTPDL 374
Db 472 XPGMSRSPDL 481

RESULT 8
ALU7_HUMAN
ID ALU7_HUMAN STANDARD: PRT: 593 AA.
AC P39194;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alu subfamily S9 sequence contamination warning entry.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95021758; PubMed=7935834;
RA Claverie J.-M.; Makalowski W.;
RT "Alu alert.";
RL Nature 371:752-752(1994).
RN [2]
RP CONCEPT.
RX MEDLINE=92241891; PubMed=1572661;
RA Claverie J.-M.;
RT "Identifying coding exons by similarity search: alu-derived and other
RT potentially misleading protein sequences.";
RL Genomics 12:838-841(1992).
RN [3]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=88333009; PubMed=3138422;
RA Quentin Y.;
RT "The Alu family developed through successive waves of fixation
RT closely connected with primate lineage history.";
RL J. Mol. Evol. 27:194-202(1988).
RN [4]
RP ALU FAMILIES CLASSIFICATION.
RX MEDLINE=91178815; PubMed=1706781;
RA Jurka J.; Milosavljevic A.;
RT "Reconstruction and analysis of human Alu genes.";
RL J. Mol. Evol. 32:105-121(1991).
CC -1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC REPEATS.
CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC CODON, 'xxx' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.

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CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC ACID SEQUENCES.
CC -1- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
CC LINKED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC BEING REPORTED.
CC -1- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC CODING NUCLEOTIDE SEQUENCE.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U14573; NOT_ANNOTATED_CDSS.
CC DR Hypothetical protein.
CC KW DOMAIN 1
CC FT DOMAIN 101 196 FRAME-1.
CC FT DOMAIN 200 295 FRAME-2.
CC FT DOMAIN 299 395 FRAME-3.
CC FT DOMAIN 399 494 FRAME-4.
CC FT DOMAIN 498 593 FRAME-5.
CC FT DOMAIN 593 644 FRAME-6.
CC SQ SEQUENCE 593 AA: 64417 MW: 544450F3JA6089F CRC64:

Query Match 16.2%; Score 330.5; DB 1; Length 593;
Best Local Similarity 45.9%; Pred. No. 5.2e-22;
Matches 89; Conservative 9; Mismatches 53; Indels 43; Gaps 7;

QY 4 SLLPRLGCGAISAHNRNLRLPGSSDSPASASRVAGITGCMCHARLIYFLVEMEPFLH 63
Db 405 SLLPRLGCGAISAHNRNLRLPGSSDSPASASRVAGITGCMCHARLIYFLVETGFHHV 463
QY 64 GQAGLEPTSDPSVSASOSARYRTG--HHARLCLANFCGRNRVSLMCPMS----- 113
Db 464 GQAGLELLTSGPPASASOSAGI-TGVSHRAR---XXXFEFERFSPSCGMSAVARSRLT 519
QY 114 -----PELKOSTCTLSLPCWMDYRRAAVGCLFLFLRHRCPPLTDEVQWCDH 161
Db 520 ATSASRVOAILLPOPEXGLQAP-----ATTGEXFLYFXRRGFTMLAR----- 564
QY 162 SLSQSTPEIKHP 175
Db 565 -LVSNSXPOVTHP 577

RESULT 9
NEK4_HUMAN
ID NEK4_HUMAN STANDARD: PRT: 841 AA.
AC P51957;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase NEK4 (EC 2.7.1.37) (NIMA-related
DE protein kinase 4) (Serine/threonine protein kinase 2)
DE (Serine/threonine-protein kinase NRK2).
GN NEK4 OR STK2.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=9426838; PubMed=8208544;
 RA Levedakou E.N., He M., Baptist E.W., Craven R.J., Cance W.G.,
 RA Weissh P.L., Simmons A., Naylor S.L., Leach R.J., Lewis T.B.,
 RA Bowcock A., Liu E.T.;
 RT "Two novel human serine/threonine kinases with homologies to the cell
 cycle regulating Xenopus Mo15, and NIMA kinases: cloning and
 characterization of their expression pattern.";
 RT Oncogene 9:1977-1988(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nucleus (Probable).
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADULT HEART, FOLLOWED BY
 CC PANCREAS, SKELETAL MUSCLE, BRAIN, LIVER, KIDNEY, LUNG AND
 CC PLACENTA. PRESENT IN MOST PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIMA SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: L20321; AAA36568.1; -
 CC DR HSSP: 063450; 1A06.
 CC DR Genew: HGNC:11399; NEK4.
 CC DR MIM: 601959;
 CC DR InterPro: IPR000719; Ser_pkinase.
 CC DR InterPro: IPR002290; Ser_thr_pkinase.
 CC DR Pfam: PF00069; pkinase; 1.
 CC DR ProDom: PD000001; Euk_pkinase; 1.
 CC DR SMART: SM00220; S_TKC; 1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferase: Serine/threonine-protein kinase; ATP-binding; Mitosis;
 CC KW Nuclear protein; Phosphorylation.
 CC FT DOMAIN 6 261 PROTEIN KINASE.
 CC FT NP_BIND 12 20 ATP (BY SIMILARITY).
 CC FT BINDING 35 35 ATP (BY SIMILARITY).
 CC FT ACT_SITE 131 131 BY SIMILARITY.
 CC FT MOD_RES 165 165 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 CC FT SEQUENCE 841 AA; 94571 MW; 0DD31920DEFEA58 CRC64;
 SQ
 Query Match 7.9%; Score 161; DB 1; Length 841;
 Best Local Similarity 46.2%; Pred. No. 1,1e-06;
 Matches 42; Conservative 14; Mismatches 25; Indels 10; Gaps 4;
 OY 6 LIPRLCNGAISAHNRNLPLGSSSDPASASVAVGTCGCTHAR-LILYFLVEMEFHYHG 64
 DB 460 LSPRLCEGSLTILASNLRLGSSSDPASASVAVGTCGCTHARQVAVGECIEKQ----G 515
 OY 65 QAGLELP---TSDDPSVAS--QSARRTGH 90
 DB 516 RIHPDLOPHNGSSEPSLSRORRORRROTET 546
 RESULT 10
 SCGE_HUMAN
 ID SCGE_HUMAN STANDARD; PRT; 438 AA.
 AC 043556;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Epsilon-sarcoglycan precursor (Epsilon-Sg).
 GN SCGE OR ESG.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RA Nigro V.;
 RA Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=98133310; PubMed=9475163;
 RA McNally E.M., Ly C.T., Kunkel L.M.;
 RT "Human epsilon-sarcoglycan is highly related to alpha-sarcoglycan
 RT (adhalin), the limb girdle muscular dystrophy 2D gene.";
 RL FEBS Lett. 422:27-32(1998).
 RN [3]
 RP SEQUENCE OF 269-413 FROM N.A.
 RX MEDLINE=98070432; PubMed=9405466;
 RA Ettinger A.J., Feng G., Sanes J.R.;
 RA Ettinger A.J., Feng G., Sanes J.R.;
 RT "Epsilon-sarcoglycan, a broadly expressed homologue of the gene
 RT mutated in limb-girdle muscular dystrophy 2D.";
 RL J. Biol. Chem. 272:32534-32538(1997).
 RN [4]
 RP ERRATUM.
 RA Ettinger A.J., Feng G., Sanes J.R.;
 RL J. Biol. Chem. 273:19922-19922(1998).
 CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF
 CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE
 CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Sarcolemma
 CC (Potential).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SCGE-1 (SHOWN HERE) AND SCGE-2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF031920; AAC14021.1; ALT_INIT.
 CC DR EMBL: AF036364; AAC04368.1; -
 CC DR EMBL: AJ000534; CA004167.1; -
 CC DR Genew: HGNC:10808; SCGE.
 CC DR MIM: 604149; -
 CC DR KMW Cytoskeleton; Transmembrane; Glycoprotein; Signal;
 CC KW Alternative splicing
 CC FT CHAIN 23 438
 CC FT DOMAIN 23 293
 CC FT TRANSMEM 294 314
 CC FT DOMAIN 315 438
 CC FT DOMAIN 211 317
 CC FT CARBOHYD 176 176
 CC FT VARSPIC 395 419
 CC FT SEQUENCE 438 AA; 49754 MW; D87D1899E9C16F23 CRC64;
 SQ
 Query Match 5.0%; Score 101.5; DB 1; Length 438;
 Best Local Similarity 29.0%; Pred. No. 0.11;
 Matches 29; Conservative 7; Mismatches 25; Indels 39; Gaps 3;
 OY 155 EYWCDSHSLDPSTPEIKH-----PPASASVAGTKD--M 187
 DB 331 DIQLVHNSAIQKSTFLRDMSKNREIAMPSTLPVPHVPTGRIIPPLHTDWDSTNPLM 390
 OY 188 HHYTWLFIFFINFLRQSLNSTYQAGVQWRNIGSLQPLRP 227

DB 391 QTCQM-----SFAPVAGVQVMDLGLQPPPP 418

RESULT 11

MTOL_HUMAN

ID MTOL_HUMAN STANDARD: PRT: 717 AA.

AC Q9Y222; Q8W257; Q9BS06; Q96FE6;

DT 30-MAY-2000 (Rel. 39, Created)

DR 15-JUN-2002 (Rel. 41, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE MTOL protein homolog (Protein CGT-02).

GN MTOL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 5).

RX MEDLINE=20272150; PubMed=10810093;

RA Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 5 AND 6).

RC TISSUE=Lymph, and Placenta;

RA Strausberg R.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

CC -1- ALTERNATIVE PRODUCTS: 5 isoforms: 1, 2, 3/4 (shown here), 5 and 6;

CC are produced by alternative splicing.

CC -1- SIMILARITY: BELONGS TO THE GIDA FAMILY.

CC -1- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 9.

CC

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CC -----

DR EMBL: AF132937; AAD27712.1; ALT_FRAME.

DR EMBL: AF469110; AAL82394.1; -.

DR EMBL: AF469111; AAL82395.1; -.

DR EMBL: AF442963; AAL35894.1; -.

DR EMBL: AF319422; AAG42814.3; -.

DR EMBL: AY078986; AAL85491.1; -.

DR EMBL: AY078985; AAL85490.1; -.

DR EMBL: BC005808; AAH05808.1; -.

DR EMBL: BC011051; AAH11051.1; ALT_INIT.

DR InterPro: IPR002218; GIDA.

DR InterPro: IPR004416; GIDA_sub.

DR Pfam: PF01134; GIDA.1.

DR ProDom: PD003738; GIDA.1.

DR TIGRfam: TIGR00136; gida.1.

DR PROSITE: PS01280; GIDA.1; 1.

DR PROSITE: PS01281; GIDA.2; 1.

DR Alternative splicing.

FT VARSPLIC 1 74 MISSING (IN ISOFORM 6).

FT VARSPLIC 179 275 MISSING (IN ISOFORM 1).

FT VARSPLIC 314 717 MISSING (IN ISOFORM 2).

FT VARSPLIC 376 400 MISSING (IN ISOFORM 1 AND ISOFORM 5).

FT CONFLICT 300 300 H -> Q (IN REF. 1 AND 2; AAL82394/AAL82395).

FT CONFLICT 586 587 LA -> CT (IN REF. 2; AAL35894).

FT SEQUENCE 717 AA: 79963 MW: 78F84DB883BCED3 CR664;

Query Match 5.0%; Score 101; DB 1; Length 717;

Best Local Similarity 86.4%; Pred. No. 0.22;

Matches 19; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LLLPRLCNGAISAHNRLPLPG 26

DB 381 LLLPRLCNGAISAHNRLPLPG 402

RESULT 12

2195_HUMAN

ID 2195_HUMAN STANDARD: PRT: 629 AA.

AC 014628;

DT 15-JUL-1998 (Rel. 36, Created)

DR 15-JUL-1998 (Rel. 36, Last sequence update)

DE 15-OCT-2001 (Rel. 40, Last annotation update)

DE Zinc finger protein 195.

GN ZNF195 OR ZNFPI04.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.

RX MEDLINE=98008942; PubMed=9344677;

RA Hussey D.J., Parker N.J., Hussey N.D., Little P.F.R., Dobrovic A.;

RL "Characterization of a KRAB family zinc finger gene, ZNF195, mapping to chromosome band 11p15.5.";

RL Genomics 45:451-455(1997).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHOWN HERE), B AND C: ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT HEART, BRAIN, PLACENTA, SKELETAL MUSCLE AND PANCREAS, AND IN FETAL LUNG, KIDNEY AND BRAIN.

CC THERE IS LITTLE EXPRESSION IN ADULT LUNG, LIVER AND KIDNEY.

CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

CC

CC -1- SIMILARITY: CONTAINS 1 KRAB DOMAIN.

CC

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CC -----

DR EMBL: AF003540; AAB86596.1; -.

DR HSSP: P08046; 1AIG.

DR GeneW: HGNC:12986; ZNF195.

DR MIM: 602187; -.

DR InterPro: IPR001909; KRAB.

DR InterPro: IPR000822; znf_C2H2.

DR Pfam: PF00096; zf_C2H2; 9.

DR Pfam: PF01352; KRAB.1.

DR PRINTS: PRO0048; ZINC_FINGER.

DR ProDom: PD000003; znf_C2H2; 9.

DR SMART: SM00349; KRAB.1.

DR SMART: SM00355; znf_C2H2; 9.

DR PROSITE: PS50805; KRAB.1.

DR PROSITE: PS50028; ZINC_FINGER_C2H2_1; 9.

DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 10.

DR Zinc-finger: Metal-binding; DNA-binding; Nuclear protein;

DR Alternative splicing.

FT DOMAIN 4 75 KRAB.

FT DOMAIN 76 243 SPACER.

FT ZN_FING 244 266 C2H2-TYPE.

FT ZN_FING 410 432 C2H2-TYPE.

FT ZN_FING 438 460 C2H2-TYPE.

FT ZN_FING 466 488 C2H2-TYPE.

FT ZN_FING 516 544 C2H2-TYPE.

FT ZN_FING 522 544 C2H2-TYPE.

FT ZN_FING 550 572 C2H2-TYPE.

FT ZN_FING 578 600 C2H2-TYPE.

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FT 2N.FING 606 628 C2H2-TYPE
SQ SEQUENCE 629 AA: 72303 MW: D9C333FE6DBE7FE CRC64:
Query Match 4.9%; Score 100; DB 1; Length 629;
Best Local Similarity 41.0%; Pred. No. 0.23;
Matches 34; Conservative 8; Mismatches 31; Indels 10; Gaps 5;

OY 216 WRNIGS--LQPLPGFKLFC--PSLLSWPYRRPRLANFVLEVGFTMFARLIL-IS 271
DB 37 YRNLFSGVLTVCCKG--LTLEQKRPKNVYKQELADGH-----PEMGFHHATQACIELL 90
OY 272 GPCDLPASASOSAGITGVSHAR 294
DB 91 GSSDLPASASOSAGITGVNHRQ 113

RESULT 13
RED1_HUMAN STANDARD; PRT: 741 AA.
AC P78563: P78555: 000691: 000395: 000465:
DT 01-NOV-1997 (rel. 35; Last sequence update)
DT 01-NOV-1997 (rel. 35; Last sequence update)
DT 16-OCT-2001 (rel. 40; Last annotation update)
DE Double-stranded RNA-specific editase 1 (EC 3.5.-.-) (dsRNA adenosine
DE deaminase) (RNA editing enzyme 1).
GN ADAR1 OR RED1 OR DRADA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Gerber A., O'Connell M.A., Keller W.;
RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RA Miltaz L., Scott H.S., Rossier C., Antonarakis S.E.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Lai F., Chen C.X., Carter K.C., Nishikura K.;
RA "Editing of glutamate receptor B subunit ion channel RNAs by four
RA alternatively spliced DRADA2 double-stranded RNA adenosine
RA deaminases."
RL Mol. Cell. Biol. 17:2413-2424(1997).
RN 14
RP SEQUENCE FROM N.A.
RA Villard L., Tassone F., Haymowicz M., Welborn R., Gardiner K.;
RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN 15
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Tokoki Y., Choi D.-K., Soeda E.,
RA Onki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kump K., Lehmann R., Schudy A., Zimmermann W.,
RA Reichwald K., Rump A., Schillhabel M., Kawasaki K., Asakawa S.,
RA Rosenthal A., Kudoh J., Shibuya K., Mitsuyama S., Antonarakis S.E.,
RA Shintani A., Sasaki T., Nagamine K., Horisawa K., Brandt P.,
RA Minoshima S., Shimizu N., Nordisk G., Horisawa K., Brandt P.,
RA Scharte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Rammer J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehnach H., Reinhardt R., Yaspo M.-L.;
RA "The DNA sequence of human chromosome 21."
RL Nature 405:311-319(2000).
CC -!- FUNCTION: EDITING OF THE MESSENGER RNAs FOR GLUTAMATE RECEPTOR
CC (GLUR) SUBUNITS BY SITE-SELECTIVE ADENOSINE DEAMINATION. EDITS
CC BOTH THE GLUR-B/O/R AND R/G SITES EFFICIENTLY BUT CONVERTS THE
CC ADENOSINE IN HOTSPOTS MUCH LESS EFFICIENTLY.

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CC -!- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS: RED1-L/DRADA2B
CC (SHOWN HERE), RED1-S/DRADA2A AND DRADA2C; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO THE ADENOSINE DEAMINASE EDITASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 DREM (DOUBLE-STRANDED RNA-BINDING) DOMAINS.
CC
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CC
DR EMBL: 082120; AAB61686.1; -
DR EMBL: 082121; AAB61687.1; -
DR EMBL: X99227; CAA67611.1; -
DR EMBL: X99383; CAA67612.1; -
DR EMBL: U76420; AAC51240.1; -
DR EMBL: U76421; AAC51241.1; -
DR EMBL: U76422; AAC51242.1; -
DR EMBL: AF001042; AAB58300.1; -
DR EMBL: AF163301; CAB90493.1; -
DR HSSP: Q91836; IDI2.
DR Genew: HGNC:226; ADAR1.
DR MIM: 601218; -
DR InterPro: IPR002466; A.deamin.
DR InterPro: IPR001159; DS.RBD.
DR Pfam: PF00035; dsrm. 2.
DR Pfam: PF02137; A.deamin. 1.
DR SMART: SM00358; DSRM; 2.
DR PROSITE: PS50141; A.DEAMIN_EDITASE; 1.
DR PROSITE: PS50137; DS.RBD; 2.
DR mRNA processing; Hydrolase; 2.
KW mRNA processing; Hydrolase; 2.
KW Zinc; RNA-binding; Repeat;
KW Alternative splicing.
KW DOMAIN 76 146 DREM 1.
FT DOMAIN 230 300 DREM 2.
FT METAL 394 394 ZINC (BY SIMILARITY).
FT ACT_SITE 396 396 ZINC (BY SIMILARITY).
FT METAL 451 451 ZINC (BY SIMILARITY).
FT METAL 556 556 ZINC (BY SIMILARITY).
FT VARSPLIT 466 505 MISSING (IN ISOFORM DRADA2A).
FT VARSPLIT 713 741 ARLEFATKAGLGAWKPEQDOFSILTP -> VH (IN
FT ISOFORM DRADA2C).
FT CONFLICT 30 G->A (IN REF. 4).
FT CONFLICT 423 R->E (IN REF. 4).
FT CONFLICT 475 V->L (IN REF. 4).
SQ SEQUENCE 741 AA: 80763 MW: 02B583414D59C20 CRC64:
Query Match 4.8%; Score 98.5; DB 1; Length 741;
Best Local Similarity 65.7%; Pred. No. 0.37;
Matches 23; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

OY 306 SHSVQAGVQWPNLGSLOPLPGKLRFSCLSPSS 340
DB 467 SHSVQAGVQWPNLGSLOPLPGKLRFSCLSPSS 340

RESULT 14
GG2_HUMAN STANDARD; PRT: 501 AA.
ID GYG2_HUMAN
AC 015488: 015489: 015490: 015486: 015485: 015487:
DT 30-MAY-2000 (rel. 39; Last sequence update)
DT 30-MAY-2000 (rel. 39; Last sequence update)
DT 15-JUN-2002 (rel. 41; Last annotation update)
DE Glycogenin-2 (EC 2.4.1.186) (GN2).
GN GYG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

```

RC TISSUE=LIVER; PubMed=98010589; Pubmed=9346895;
RX MEDLINE=98010589; PubMed=9346895;
RA Mu J., Skurat A.V., Roach P.J.;
RT "Glycogenin-2, a novel self-glycosylating protein involved in liver
glycogen biosynthesis";
RL J. Biol. Chem. 272:27589-27597(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20184741; Pubmed=10721716;
RA Zhai L., Mu J., Zong H., Depaulis-Roach A.A., Roach P.J.;
RT "Structure and chromosomal localization of the human glycogenin-2 gene
gxc2";
RL Gene 242:229-235(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RX TISSUE=SKIN;
RA Strausberg R.;
RN Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
[4]
RP CHARACTERIZATION, AND CARBOHYDRATE-LINKAGE SITE TYR-228.
RX MEDLINE=99074257; Pubmed=9857012;
RA Mu J., Roach P.J.;
RT "Characterization of human glycogenin-2, a self-glycosylating
initiator of liver glycogen metabolism";
RL J. Biol. Chem. 273:34850-34856(1998).
RN [5]
RP MASS SPECTROMETRY.
RX TISSUE=Breast cancer;
MEDLINE=21829512; Pubmed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
protein expression map database";
RL Proteomics 2:212-223(2002).
RN [6]
RP FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
GLYCOGEN SYNTHASE.
RX CC
CC -1- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
glucosylglycogenin.
CC CC
CC -1- COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF
DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.
CC CC
CC -1- PATHWAY: Glycogen biosynthesis.
CC CC
CC -1- SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.
CC CC
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS: ALPHA (SHOWN HERE),
BETA, GAMMA, DELTA, EPSILON AND ZETA; ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC CC
CC -1- TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN LIVER, HEART, AND
PANCREAS.
CC CC
CC -1- PTM: SELF-GLUCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM
UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10
RESIDUES ATTACHED TO TYR-228.
CC CC
CC -1- MASS SPECTROMETRY: MW=55211.89; METHOD-MALDI.
CC CC
CC -1- SIMILARITY: BELONGS TO THE GLYCAGENIN FAMILY.

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or send an email to license@isb-sib.ch).
CC
DR EMBL: U94362; AAB84377.1; -
DR EMBL: U94363; AAB84378.1; -
DR EMBL: U94364; AAB84379.1; -
DR EMBL: U94357; AAB84373.1; -
DR EMBL: U94358; AAB84374.1; -
DR EMBL: U94360; AAB84375.1; -
DR EMBL: U94361; AAB84376.1; -
DR EMBL: AF179624; AAFF61855.1; -
DR EMBL: AF179615; AAFF61855.1; JOINED.
DR EMBL: AF179616; AAFF61855.1; JOINED.

DR	EMBL; AF179617;	AAFG1855.1;	JOINED.
DR	EMBL; AF179618;	AAFG1855.1;	JOINED.
DR	EMBL; AF179619;	AAFG1855.1;	JOINED.
DR	EMBL; AF179620;	AAFG1855.1;	JOINED.
DR	EMBL; AF179621;	AAFG1855.1;	JOINED.
DR	EMBL; AF179622;	AAFG1855.1;	JOINED.
DR	EMBL; AF179623;	AAFG1855.1;	JOINED.
DR	EMBL; BC03152;	AAH23152.1;	-
DR	GeneW; HGNC:4700;	GTG2.	
DR	MIM; 300198;	-	
DR	InterPro; IPR002495;	GT-8.	
DR	Pfam; PF01501;	Glyco transf.8; 1.	
KW	Transferrase; Glycogen biosynthesis;	Alternative splicing;	
KW	Glycoprotein; Polymorphism.		
FT	ACT_SITE	119 .. 119	BY SIMILARITY.
FT	CARBOND	228 .. 228	O-LINKED (GLC. . .)
FT	VARSPLIC	3 .. 33	MISSING (IN ISOFORM BETA).
FT	VARSPLIC	3 .. 42	MISSING (IN ISOFORM GAMMA).
FT	VARSPLIC	378 .. 448	MISSING (IN ISOFORM DELTA).
FT	VARSPLIC	407 .. 501	MISSING (IN ISOFORM EPSILON).
FT	VARSPLIC	413 .. 448	MISSING (IN ISOFORM ZETA).
FT	VARIANT	270 .. 270	V -> A.
FT	MUTAGEN	228 .. 228	/FtID=VAR_010401.
FT	MUTAGEN	230 .. 230	Y->E: LOSS OF ACTIVITY.
FT	CONFLICT	313 .. 313	Y->F: NO LOSS OF ACTIVITY.
FT	CONFLICT	413 .. 413	H -> R (IN REF. 3).
FT	CONFLICT	462 .. 464	MISSING (IN REF. 1; AAB84378).
FT	CONFLICT	464 .. 464	EKV -> AGI (IN REF. 1; AAB84376).
SO	SEQUENCE	501 AA; 55211 MW; 2BDE05FDAD5A7657 CRC64;	
<hr/>			
Query Match 4.8%; Score 98; DB 1; Length 501;			
Best Local Similarity 19.6%; Pred. No. 0.27; Mismatches 100; Indels 230; Gaps 22			
<hr/>			
DQ	57 EMEFLHWQAQDELPTSDPSVASOSARYRTGHNRALDN--- <td>100</td> <td></td>	100	
DQ	3 ETEFHNGAQADELLRSLNSPSTASQSAGMTVTDQAFATLATNDYICGGALVLGSLRRH	62	
DQ	101 --GNRVSLMCRSPWS-----	125	
DQ	63 RLTRKLIVLIPROVSLLRWLSKVFDEVIEVNLIDSADYTHLAFLKRPELG---LTLT	118	
DQ	126 K--CW-----DYRAAAY-----GFLEFLLRHR	147	
DQ	119 KLHCPTTLTHSKCYFLDADTLVLSNVDELFRGEESAARDGWPCDFSGVFWTOPSLHT	178	
DQ	148 CPTLPDEVMQCDHSLOPSTRTEIKNPASASOVAGTKDMNYTULFIETFNFLROSIN	207	
DQ	179 HKLLLDNM---EHCSFGDAQGLN---SFRKNSTDTDIKH---LPIYNLSSNTMY	228	
DQ	208 SVTQAGVQWRN-----LGSLOPLRPFGFKLFSCPSLLSMWDYRRPPRLANFFVFLVEMG	260	
DQ	229 TYPAPFKQFGSSAKVNHFLGSMKP-----WNKYKNPQSGS---VLBOG	268	
DQ	261 -----FTMFALLIL-----ISGCDDLPASASQ	282	
DQ	269 SVSSSQHOAQLHLMTWTYYNNVLYRLXSVQAGEARAASPGHTLCHSDVGRC----	323	
DQ	283 SAGITGVSHHARLIENFCLFEHESHSYTQAGVOMPN--LGSLOP-----	324	
DQ	324 ASGVG-----EPCKNSTPSAGVPCANSPLSGSNQRQGLRPETPOIVDETLS	368	
DQ	325 LRPGLGR-----FSC--LSLPSMDYGHLRPHRAPN	353	
DQ	369 LPGRHRSMDMIACPETETPAVITOCPLSQPS-----PDPADE	405	
<hr/>			
RESULT 15			
RPRO_NMV	STANDARD:	PRT:	1643 AA.
ID_RPRO_NMV			
AC_P15095:			
DT 01-APR-1990 (Rel. 14, Created)			
DT 01-APR-1990 (Rel. 14, Last sequence update)			

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA replication protein (186 kDa protein) (ORF 1) [Contains: RNA-
directed RNA polymerase (EC 2.7.7.48); Probable helicase].
OS Narcissus mosaic virus (NMV).
CC Viruses; ssRNA positive-strand viruses, no DNA stage; Potexvirus.
OX NCBI_TaxID=12180;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89279206; PubMed=2732689;
RA Zuidema D., Linthorst H.J.M., Huisman M.J., Asjes C.J., Bol J.F.;
RT "Nucleotide sequence of narcissus mosaic virus RNA.";
RU J. Gen. Virol. 70:267-276(1989).
CC -!- FUNCTION: RNA-replication. The central part of this protein
possibly functions as an ATP-binding helicase.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
[RNA](N).

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CC EMBL: D13747; BAA02891.1; -
DR PIR: J0470; RRGWNV.
DR InterPro: IPR001788; RNA_dep_RNAPol2.
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF00978; RNA_dep_RNAPol2; 1.
DR Pfam: PF01443; Viral_helicase1; 1.
KW ATP-binding; Helicase; RNA replication; RNA-directed RNA polymerase;
transferrase.
KW NP_BIND 868 875 ATP (POTENTIAL).
SQ SEQUENCE 1643 AA; 186304 MW; ADA6EFC0FE2EC43 CRC64;

Query Match 4.7%; Score 96.5; DB 1; Length 1643;
Best Local Similarity 20.6%; Pred No. 1.4; Mismatches 113; Indels 95; Gaps 14;
Matches 64; Conservative 39;

QY 100 CGRNRVSLMCPSPSPKSLKSTCLSLPKCWYRRAVPGFLIFLIRHRCPTLTQDEVQMC 159
DB 869 CGSGCKSFALQEMMRSLKEDQSVV-----TVVTPVLLRNDMQTKLPILPADVFKTF 920
QY 160 DHSSLOPSTPEI-----KHPPASQVAGTKDMHHYTLIFLIFENLRQSLNSVTQAG 213
DB 921 EKSVIOPCNPIVDDYTKLPGLIESV---MHON-VFILLGDNKQSVYHETNPE 975
QY 214 VQWRNLGSLQPLPPGFKLFS--CPSLSSWDYRRPRLANFVFLVEMGFTMFARLLILS 271
DB 976 AV-----IALPENVEIFSPYCEFLNA-THRNVKDLAN-----KLGV----- 1012
QY 272 GPDDLPAASQASAG--ITGVSHHAR-----LIFNCLFEMESHSVTQAGVQMPN 318
DB 1013 -----YSEREGKLVKVNFAASHLKAIRIPMLVPTMKRNAMFDMGHSMYAGQGLT 1064
QY 319 LGSLOPLPPGLKRF-----SCLSL-----PSSWDYGHLPHPANECIFIRGC 360
DB 1065 APKIQILLNHTQFCSEKRVLYTCLSRVRIHFINTGPTTGDY-----WAKLE 1112
QY 361 VSPYLSGWSQT 371
DB 1113 STPYLAKAFIDT 1123

Search completed: July 17, 2003, 18:17:53
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 17, 2003, 18:15:09 ; Search time 40 seconds
(without alignments)
901.260 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MEFLSLPRLCNGAISAHK.....FIRGVSPLYSGMSQTPDLR 375

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382.5	18.8	673	4 F40201	artifact-warning s
2	315.5	15.5	613	4 C40201	artifact-warning s
3	315.5	15.5	627	4 A40201	artifact-warning s
4	291.5	14.3	597	4 D40201	artifact-warning s
5	197.5	9.7	579	4 D40201	artifact-warning s
6	175	8.6	499	2 S65657	alpha-1C-adrenegrl
7	167	8.2	46	2 I54375	gene NF2 protein
8	161	7.9	841	1 I78885	serine/threonine-s
9	157	7.7	39	2 I54374	gene NF2 protein
10	151.5	7.4	301	4 B40201	artifact-warning s
11	139.5	6.9	100	2 A46010	X-linked retinopat
12	137.5	6.8	79	2 A56194	thromboxane A-2 re
13	137.5	6.8	407	2 T02670	probable thromboxa
14	128	6.3	53	2 A42442	integrin beta-1 ch
15	112	5.3	440	2 A26359	decay-accelerating
16	106.5	5.2	1125	2 T19193	hypothetical prote
17	105	5.2	522	2 T08711	gamma-adaptin homo
18	102.5	5.0	331	2 S59501	interferon recepto
19	99.5	4.9	331	2 A54295	interferon alpha/b
20	96.5	4.7	1643	1 RRMGNV	genome polypeptid
21	96	4.7	458	2 E82175	conserved hypotet
22	92	4.5	964	2 T15342	transcription fact
23	91.5	4.5	542	2 S36749	transcription fact
24	91.5	4.5	631	1 RRMPTM	genome polypeptid
25	90.5	4.4	282	1 SAVL64	middle surface ant
26	90.5	4.4	832	1 S20752	DNA-directed DNA p
27	90.5	4.4	832	1 SAVL64	large surface anti
28	90	4.4	431	1 SAVL64	probable xylogluca
29	89	4.4	299	2 F84785	

30	89	4.4	333	2 A12131	hypothetical prote
31	88	4.4	1162	2 B97852	hypothetical prote
32	88	4.3	209	2 J04244	heat-shock 27k pro
33	88	4.3	726	2 S18208	radphillin-3A-inter
34	88	4.3	832	2 S71785	DNA-directed DNA p
35	87.5	4.3	494	2 S39607	transcription fact
36	87	4.3	226	1 J01574	major surface anti
37	87	4.3	226	1 J02101	surface antigen -
38	87	4.3	470	2 T05258	glycine hydroxymet
39	87	4.3	1153	2 A49676	nitric-oxide synth
40	86.5	4.3	360	2 T45956	hypothetical prote
41	86.5	4.3	1886	2 S04921	nuclear pore prote
42	86	4.2	262	2 AF2291	hypothetical prote
43	86	4.2	625	2 E96721	hypothetical prote
44	85.5	4.2	832	1 J01574	DNA-directed DNA p
45	84.5	4.2	191	2 C72455	hypothetical prote

ALIGNMENTS

RESULT 1									
F40201									
artifact-warning sequence (translated ALU class F) - human									
C:Species: Homo sapiens (man)									
C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #ext_change 19-May-2000									
C:Accession: F40201									
R:Claverie, J.M.									
personal communication, 1992									
A:Reference number: A40201									
A:Accession: F40201									
A:Molecule type: DNA									
A:Residues: 1-673 <CLA>									
R:Claverie, J.M.									
Genomics 12, 838-841, 1992									
A:Title: Identifying coding exons by similarity search: Alu-derived and other potenti									
A:Reference number: A40200; MUID:92241891; PMID:1572661									
A:Contents: annotation									
C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames o									
In-frame stop codons are shown as 'X'.									
C:Comment: Any significant similarity of a predicted protein sequence to a portion of									
Query Match									
Best Local Similarity 18.8%; Score 382.5; DB 4; Length 673;									
Matches 128; Conservative 19; Mismatches 111; Indels 127; Gaps 17;									
QY	16	ISAHNRLRLPGSSDPSASAPVAGITGCTHARLILYFLVEMEFHVGQAGLEPTSD	75						
DB	371	VLHCSLNLGSSDPSASVRAGITGMRHMLI-YVLIETQFHVQDAGLKLTSSD	429						
QY	76	PSVASQSARVYRTGHHARLCLANFCGRNVSIMCPSWSE-LKOSTCLSLPKCMDYRAA	134						
DB	430	-----LPSMSPKVLGXQXAXATTPTSPXXXP-V	453						
QY	135	VGGFLIFLFL-----RHRCP---TLTQDEVQMCSSLSQPEPTPEIKHPASA	178						
DB	454	FGGFFFFPALFLRLXALALALPRLCCSGKFWLTAASTSW-QAILPLSPVXGLQAWA	512						
QY	179	SOVAGT---KDMHHTWLIFFIFNFIROSLSNVTQAGVQRNIGSLQPLPPGFRLFSC	234						
DB	513	A-IPGKFMVFXRHSHTMLI-----RLVNSKXQV-----ICPPG-----	546						
QY	235	PELLSSWDYR-PRLANFEVFLVEMGFMAFLILISGCDLPAASQASAGITGVSHHA	293						
DB	547	--LPKCMDDRRPPHPAXXXLFL--GVFF-----	572						
QY	294	RLIFNCLFEMESHVSTQGVQW---PNIQSLOPLPGLKRSCLSPSSNDYGHLPHP	350						
DB	573	--FLLCFCEFXDRPLXHPG--WSAVASFGSLQPPGPKRPSCLCLPSNDYRHGPPPL	628						
QY	351	ANFCIFIRGVSPLYSGMSQTPDLR	375						

Db 629 ANLCIFNBDTVSPCXSGWSQTPDLK 653

RESULT 2

artifact-warning sequence (translated ALU class C) - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: C40201

R:Claverie, J.M.

personal communication, 1992

A:Reference number: A40201

A:Accession: C40201

A:Molecule type: DNA

A:Residues: 1-613 <CL>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential

A:Reference number: A40200; MUID:92241891; PMID:1572661

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c

in-frame stop codons are shown as 'x'.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 15.5%; Score 315.5; DB 4; Length 613;

Best Local Similarity 33.4%; Pred. No. 5.6e-20;

Matches 98; Conservative 9; Mismatches 73; Indels 113; Gaps 8;

OY 6 LLPLRECGAISAHRNLRPGSSDSPAASAPVAGITGCTHARLLTFLVEMEFLLHVGQ 65

Db 424 LSPRLCEGSAISHCKLRLPGICHSAPAFVCRGTGARTMPS-XFFVFLVEMGCHVQ 482

OY 66 AGLEPTSDSDSVASQSAARYRTGHHARLCLANFCGRNRVSLMCPMSBELKOSTCLSLP 125

Db 483 AGLELLAS-----XSTHLCCLP 498

OY 126 KCMWYRR---AAVGLFLFELRHRCPTLTODEVOMCHDSLSLOSTPEIKHPASA--- 178

Db 499 KCMWYRRRLPHAPAXXFFEFF-----XDRSLC-----HFGSMAAR 536

OY 179 SOVAGTKMHHTWLIFFITNFKQSLNSVTQACVQWRNIGSLQPLDPGKFLFSCPSLL 238

Db 537 SRLTASSTRYVAIL-----PQSAVVGLOAPA-- 565

OY 239 SSMWYRRPRLANFEVLVEMGFTMARLLISGDCDLPASASAGITGVSH 291

Db 566 -----PCPANFLYFXKMGFAMLARLVNSMWPDPPTASASAGITGVSH 610

RESULT 3

artifact-warning sequence (translated ALU class A) - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: A40201

R:Claverie, J.M.

personal communication, 1992

A:Reference number: A40201

A:Accession: A40201

A:Molecule type: DNA

A:Residues: 1-627 <CL>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potential

A:Reference number: A40200; MUID:92241891; PMID:1572661

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames of c

in-frame stop codons are shown as 'x'.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of th

Query Match 15.5%; Score 315.5; DB 4; Length 627;

Best Local Similarity 33.4%; Pred. No. 5.6e-20;

Matches 98; Conservative 9; Mismatches 73; Indels 113; Gaps 8;

OY 6 LLPLRECGAISAHRNLRPGSSDSPAASAPVAGITGCTHARLLTFLVEMEFLLHVGQ 65

Db 424 LSPRLCEGSAISHCKLRLPGICHSAPAFVCRGTGARTMPS-XFFVFLVEMGCHVQ 482

OY 66 AGLEPTSDSDSVASQSAARYRTGHHARLCLANFCGRNRVSLMCPMSBELKOSTCLSLP 125

Db 483 AGLELLAS-----XSTHLCCLP 498

OY 126 KCMWYRR---AAVGLFLFELRHRCPTLTODEVOMCHDSLSLOSTPEIKHPASA--- 178

Db 499 KCMWYRRRLPHAPAXXFFEFF-----XDRSLC-----HFGSMAAR 536

OY 179 SOVAGTKMHHTWLIFFITNFKQSLNSVTQACVQWRNIGSLQPLDPGKFLFSCPSLL 238

Best Local Similarity 33.4%; Pred. No. 5.7e-20;

Matches 98; Conservative 13; Mismatches 67; Indels 115; Gaps 7;

OY 6 LLPLRECGAISAHRNLRPGSSDSPAASAPVAGITGCTHARLLTFLVEMEFLLHVGQ 65

Db 436 LSPRLCEGSAISHCKLRLPGSRHSPASASQVAGTGTARTPG-XFFVFLVETGFHRSQ 494

OY 66 AGLEPTSDSDSVASQSAARYRTGHHARLCLANFCGRNRVSLMCPMSBELKOSTCLSLP 125

Db 495 DGLDLLT-----SXSAAR-----LCCLP 510

OY 126 KCMWYRAAVPGLFIFLFLRHRCPTLTODEVOMCHDSLSLOSTPEIKHPASASQVATK 185

Db 511 KCMWYRRETARG----- 522

OY 186 DMHHTWLIFFIF-----NFLRQSLNSVTQ---AGVQWRNIGSLQPLDPGKFLFSCPS 236

Db 523 ---XXFFLFFVFIFFPDGVSICRQGSAAVARSRLTASASRVHAILLPQPKXLGLQAPA 579

OY 237 LSSMDYRRPRLANFEVLVEMGFTMARLLISGDCDLPASASAGITGV 289

Db 580 L-----RPAFLYFXKRGFTVVAARMVISXPRDPALASASAGITGV 622

RESULT 4

E40201

artifact-warning sequence (translated ALU class E) - human

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 11-Aug-1995 #text_change 19-May-2000

C:Accession: E40201

R:Claverie, J.M.

personal communication, 1992

A:Reference number: A40201

A:Accession: E40201

A:Molecule type: DNA

A:Residues: 1-597 <CL>

R:Claverie, J.M.

Genomics 12, 838-841, 1992

A:Title: Identifying coding exons by similarity search: Alu-derived and other potenti

A:Reference number: A40200; MUID:92241891; PMID:1572661

A:Contents: annotation

C:Comment: This "warning" entry is a conceptual translation in all 6 reading frames o

in-frame stop codons are shown as 'x'.

C:Comment: Any significant similarity of a predicted protein sequence to a portion of

Query Match 14.3%; Score 291.5; DB 4; Length 597;

Best Local Similarity 30.5%; Pred. No. 7.2e-18;

Matches 118; Conservative 24; Mismatches 106; Indels 139; Gaps 20;

OY 5 LLPLRECGAISAHRNLRPGSSD-SPASAPVAGITGCTHARLLTFLVEM 58

Db 310 LLPLPEYDGTISP--QTLPGFKQFSPVASRAVAGTGMHHAQLLYFXKMGFSMLV 367

OY 59 EFLHVGQAGLEPLTSDSDSVASQSAARYRT-----GHHARLC 95

Db 368 KLVSNSQVQVIRPALNSQAGIT-GMSHTWXXKXFFPETEFECSCCPRSTMAQSHRLC 426

OY 96 LANFCGRNRVSLMCPMSBELKOSTCLSPKCMWYRRRAVPGLLFLFLRHRCPTLTODE 155

Db 427 ---FLGSSNSLSLP--PEX-----LGLQAC-----ATPSXPIYIF-----SRDG 461

OY 156 V-----QKCHDSLSQSTPEIKHPASASQVAGTKDMHHTWLIFFITNFKQSLNSVT 210

Db 462 VSPCWSWSQTPNLRKXSAAPXT-PRALGLQAXATTP-----GXKXFFLRFSFALVA 512

OY 211 QAGVQWRNIGSLQPLDPG-----KLFCPSLLSSMDYR--PPRLANFEVLVEMGFTME 264

Db 513 QAGVRMHLTA-----NFASVQAIIISCLSPSSMDYRRAPPPAN-FLFLVEMGFL-- 563

OY 265 ARLLISGDCDLPASASAGITGVSHHARLIFNFCLEFMESHSVTQAGVQWRNIGSLQ 324

Db 564 -----HYGAGAGLKLPTSGD--- 577


```
QY      66 AGLELPTSDDPVSVA 80
      11::1 :1:1
Db      60 AGVQLPFEPPTGKA 74
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RESULT 13
T02670
probable thromboxane A2 receptor isoform beta - human

Query Match	6.88	Score 137.5	DB 2	Length 407
Best Local Similarity	49.38	Pred. NO. 0.00019		
Matches 37; Conservative	8	Mismatches 25	Indels 5	Gaps 2

```
QY      66 AGLELPTSDDPSSVA 80
      ||::| : | : |
Db     388 AGVQLLPFEPPTGKA 402
```

RESULT 14
A:2442 A42442
Integrin beta-1 chain, splice form beta-1-S - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text-change 20-Aug-1999
C:Accession: A42442
R:Languiño, L.R.; Ruoslahti, E.
J. Biol. Chem. 267, 7116-7120, 1992
A:Title: An alternative form of the integrin beta 1 subunit with a variant cytoplasmic c
A:Reference number: A42442; MUID:92202279; PMID:1551917
A:Accession: A42442
A:Molecule type: mRNA
A:Residues: 1-53 <L>A>
A:Cross-references: GB:M84237; NID:g186221; PIDN:AAA74403.1; PID:g186223
A:Note: sequence extracted from NCBI backbone (NCBIN:92159, NCBI:P.92160)
C:Genetics:
A:Gene: GDB:ITGB1; FMRB
A:Cross-references: GDB:118732; OMIM:135630
A:Map position: 10p11.2-10p11.2
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: alternative splicing; duplication; heterodimer; membrane protein

[illegible]

RESULT 15
A26359
decay-accelerating factor, splice form 1 precursor - human
N:Alternate names: decay-accelerating factor 5; decay-accelerating factor secreted form

C:Species: Homo sapiens (man)
C:Date: 05-Oct-1988 #sequence-revision 05-Oct-1988 #text-change 02-Jun-2000
C:Accession: A26359; A519702; S16187; S21318; A27258
R:Caras, I.W.; Daultz, M.A.; Rhee, L.; Weddell, G.; Martin Jr., D.W.; Nussenzweig, V.
Nature 325, 545-549, 1987
A:Title: Cloning of decay-accelerating factor suggests novel use of splicing to generate
A:Reference number: A26359; MUID:87115845; PMID:2433596
A:Accession: A26359

Query match	5.58;	Score 112;	DB 2;	Length 440;
-------------	-------	------------	-------	-------------

QY 80 ASQSAFYRTGHHARCLANFCGRNRVSLMC-----PSWSPELKOSTCLSLPKCWDYRR 132

```

0y      133 AAVPGLEIFFLRHRCPTLTODEVOMCDHSSIQSPREIKRPRASASOVAGTKDMNHYTW 192
      |::| | |:: |

```

[illegible]

Search completed: July 17, 2003, 18:20:09
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 17, 2003, 18:16:09 ; Search time 27 Seconds
(without alignments)
408.652 Million cell updates/sec

Title: US-09-380-203-2

Perfect score: 2034

Sequence: 1 MEFSLLPRLPRLCNGAISAHNR.....FIRGVSPYLSGMSQTPDLR 375

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2034	100.0	375	2	US-08-454-557C-121
2	2034	100.0	375	2	US-08-340-426D-121
3	2034	100.0	375	2	US-08-450-673C-121
4	1415.5	69.6	397	5	PCT-US95-17111A-121
5	250	12.3	132	4	US-09-605-785-573
6	218	10.7	1079	3	US-09-058-489-22
7	210.5	10.3	110	4	US-09-227-357-193
8	186	9.1	56	4	US-09-227-357-577
9	168.5	8.3	500	4	US-09-265-630-13
10	158	7.8	122	4	US-09-227-357-285
11	155	7.6	388	4	US-09-265-630-11
12	141	6.9	90	4	US-09-227-357-171
13	129.5	6.4	99	4	US-09-288-143-168
14	128	6.3	48	3	US-08-951-200A-1
15	122	6.0	53	3	US-08-951-200A-8
16	120	5.9	72	4	US-09-227-357-655
17	109	5.4	579	3	US-08-704-711A-1
18	109	5.4	579	4	US-09-521-220-1
19	99.5	4.9	331	4	US-08-585-191A-2
20	99.5	4.9	331	4	US-08-472-402A-2
21	98.5	4.8	714	4	US-09-347-878-16
22	92.5	4.5	47	4	US-09-227-357-656
23	91.5	4.5	631	4	US-08-927-219-127
24	90.5	4.4	105	4	US-08-556-627A-4
25	89	4.4	32	4	US-09-288-143-171
26	87	4.3	630	4	US-08-927-219-2
27	87	4.3	630	4	US-08-927-219-4

28	87	4.3	1146	4	US-09-126-109-12	Sequence 12, App1
29	83	4.1	716	2	US-08-766-982-1	Sequence 1, App1
30	83	4.1	716	4	US-09-296-219-1	Sequence 1, App1
31	82.5	4.1	226	5	PCT-US86-10602-14	Sequence 14, App1
32	82.5	4.1	493	4	US-08-999-774A-12	Sequence 12, App1
33	82.5	4.1	1306	4	US-08-999-774A-13	Sequence 13, App1
34	82	4.0	544	4	US-09-087-134-14	Sequence 14, App1
35	82	4.0	655	4	US-09-228-986-70	Sequence 70, App1
36	82	4.0	1153	1	US-08-314-917-2	Sequence 2, App1
37	82	4.0	1153	1	US-08-265-046-2	Sequence 2, App1
38	82	4.0	1153	2	US-08-465-522-2	Sequence 2, App1
39	82	4.0	1153	5	PCT-US93-11401-2	Sequence 2, App1
40	82	4.0	1153	5	PCT-US95-07849-2	Sequence 2, App1
41	81.5	4.0	281	1	US-08-105-483-214	Sequence 214, App
42	81.5	4.0	281	1	US-08-709-209-214	Sequence 214, App
43	81.5	4.0	281	1	US-08-458-101-214	Sequence 214, App
44	81.5	4.0	351	5	PCT-US96-10602-4	Sequence 4, App1
45	81.5	4.0	389	1	US-08-105-483-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-08-454-557C-121
; Sequence 121, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Mandis, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 121:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-454-557C-121
Query Match 100.0%; Score 2034; DB 2; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLPRLCNGAISAHNRNLPGSSDSPASASVYAGTGTCTARLLTYFLVMEF 60
|||||
DB 1 MEFSLLPRLCNGAISAHNRNLPGSSDSPASASVYAGTGTCTARLLTYFLVMEF 60
61 LHVQAGLELPTSDPSVSASQASARYRTGHARLCLANFCGRNRVSLMCPSPFLKOST 120

|||||
Db 61 LHVQAGLELPTSDPVSASQSAARYRTGHHARLCLANFCGRNRVSLMCPSPMSELKOST 120
|||
Qy 121 CLSLPKCWDYRRAAVPGLIFLFLRHRCPTLTODEVOMCHSSLOPSTPEIKHPASASQ 180
|||
Db 121 CLSLPKCWDYRRAAVPGLIFLFLRHRCPTLTODEVOMCHSSLOPSTPEIKHPASASQ 180
|||
Qy 181 VAGTKDMHHTWLTFFIFENFLRQSLNSVTQAGVQWRNLGSLQPLPGFKLFSCPSLSS 240
|||
Db 181 VAGTKDMHHTWLTFFIFENFLRQSLNSVTQAGVQWRNLGSLQPLPGFKLFSCPSLSS 240
|||
Qy 241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIFNFC 300
|||
Db 241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIFNFC 300
|||
Qy 301 LFEMESHVSVOAGVQWPNLGSLOPLPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
|||
Db 301 LFEMESHVSVOAGVQWPNLGSLOPLPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
|||
Qy 361 VSPYLSGMSQTPDLR 375
|||
Db 361 VSPYLSGMSQTPDLR 375

RESULT 2
US-08-340-426D-121

Sequence 121, Application US/08340426D
Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-340-426D-121

Query Match 100.0%; Score 2034; DB 2: Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEFSLLPRLCEGATSAHRNRLPLGSSDSPASASPVAGITGCTHARLLIFFLVEMEF 60
|||
Db 1 MEFSLLPRLCEGATSAHRNRLPLGSSDSPASASPVAGITGCTHARLLIFFLVEMEF 60

Qy 61 LHVQAGLELPTSDPVSASQSAARYRTGHHARLCLANFCGRNRVSLMCPSPMSELKOST 120
|||
Db 61 LHVQAGLELPTSDPVSASQSAARYRTGHHARLCLANFCGRNRVSLMCPSPMSELKOST 120
|||
Qy 121 CLSLPKCWDYRRAAVPGLIFLFLRHRCPTLTODEVOMCHSSLOPSTPEIKHPASASQ 180
|||
Db 121 CLSLPKCWDYRRAAVPGLIFLFLRHRCPTLTODEVOMCHSSLOPSTPEIKHPASASQ 180
|||
Qy 181 VAGTKDMHHTWLTFFIFENFLRQSLNSVTQAGVQWRNLGSLQPLPGFKLFSCPSLSS 240
|||
Db 181 VAGTKDMHHTWLTFFIFENFLRQSLNSVTQAGVQWRNLGSLQPLPGFKLFSCPSLSS 240
|||
Qy 241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIFNFC 300
|||
Db 241 WDYRRPRLANFEVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHHARLIFNFC 300
|||
Qy 301 LFEMESHVSVOAGVQWPNLGSLOPLPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
|||
Db 301 LFEMESHVSVOAGVQWPNLGSLOPLPGKLRFSCLSLPSSWDYGHLPHPANFCIFIRGG 360
|||
Qy 361 VSPYLSGMSQTPDLR 375
|||
Db 361 VSPYLSGMSQTPDLR 375

RESULT 3
US-08-450-673C-121

Sequence 121, Application US/08450673C
Patent No. 5948888
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-450-673C-121

Query Match 100.0%; Score 2034; DB 2: Length 375;
Best Local Similarity 100.0%; Pred. No. 2.4e-215;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEFSLLPRLCEGATSAHRNRLPLGSSDSPASASPVAGITGCTHARLLIFFLVEMEF 60
|||
Db 1 MEFSLLPRLCEGATSAHRNRLPLGSSDSPASASPVAGITGCTHARLLIFFLVEMEF 60

QY	61	LHVQAGLELPTSDPSVASASQATYRGHNARILCANCGNRNYSLMQSPMSPBLKOST	120
Dp	61	LHVQAGLELPTSDPSVASASQATYRGHNARILCANCGNRNYSLMQSPMSPBLKOST	120
QY	121	CLSLPKCDYRRAAPGLFLEFLNHRCPRTLQODEVOMCDHSLQSTPEIKRPPASASQ	180
Dp	121	CLSLPKCDYRRAAPGLFLEFLNHRCPRTLQODEVOMCDHSLQSTPEIKRPPASASQ	180
QY	181	VAGTRDMHNYTWLIFLFIENFLKROSLNSTQAGVOMRNLGSIQPLRPGFKLFSCPSLSS	240
Dp	181	VAGTRDMHNYTWLIFLFIENFLKROSLNSTQAGVOMRNLGSIQPLRPGFKLFSCPSLSS	240
QY	241	WDYRRRPLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHNARLLFNFC	300
Dp	241	WDYRRRPLANFVFLVEMGFTMFARLLISGPCDLPASASQAGITGVSHNARLLFNFC	300
QY	301	LFEMESHVTOAGVOMPNLGSIQPLRPGIKRRSCLSLBSMWGYGHLRPHRPNANCFITRG	360
Dp	301	LFEMESHVTOAGVOMPNLGSIQPLRPGIKRRSCLSLBSMWGYGHLRPHRPNANCFITRG	360
QY	361	VSPLYLSGMSQTPDLR 375	
Dp	361	VSPLYLSGMSQTPDLR 375	

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1      RESULT 4
2      PCT-US95-17111A-121
3      : Sequence 121, Application PC/TUS9517111A
4      : GENERAL INFORMATION:
5      : APPLICANT: de la Monte, Suzanne
6      : APPLICANT: Wands, Jack R.
7      : TITLE OF INVENTION: Neutral Thread Protein Gene Expression and
8      : TITLE OF INVENTION: Detection of Alzheimer's Disease
9      : NUMBER OF SEQUENCES: 121
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
12     : STREET: 1100 New York Avenue, Suite 600
13     : CITY: Washington
14     : STATE: D.C.
15     : COUNTRY: U.S.A.
16     : ZIP: 20005-3934
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: Patentln Release #1.0, Version #1.25
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: PCT/US95/17111A
24     : FILING DATE:
25     : CLASSIFICATION:
26     : PRIOR APPLICATION DATA:
27     : APPLICATION NUMBER: 08/340,426
28     : FILING DATE: 14-NOV-1994
29     : ATTORNEY/AGENT INFORMATION:
30     : NAME: Ludwig, Steven R.
31     : REGISTRATION NUMBER: 36,203
32     : REFERENCE/DOCKET NUMBER: 0609,3840002
33     : TELECOMMUNICATION INFORMATION:
34     : TELEPHONE: (202) 371-2600
35     : TELEFAX: (202) 371-2540
36     : INFORMATION FOR SEQ ID NO: 121:
37     : SEQUENCE CHARACTERISTICS:
38     : LENGTH: 397 amino acids
39     : TYPE: amino acid
40     : TOPOLOGY: linear
41     : MOLECULE TYPE: protein
42     : PCT-US95-17111A-121

```

Query Match	69.68;	Score 1415.5;	DB 5;	Length 397;
Best Local Similarity	74.68;	Pred. No. 2.8e-147;		
Matches 285;	Conservative 10;	Mismatches 44;	Indels 43;	Gaps 7

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QY      1 MEFSLLEPRLECNCAISAHNRNILEGSSDSPASASPVAGITGMCJARILILEVLEMEF 60
Db      1 MEFSLLEPRLECNCAISAHNRNILEGSSDSPASASPVAGITGMCJARILILEVLEMEF 60
QY      61 LHVAGAGLEL-----PTSDPPVSASASARYRTGHNHARLCIANFCGRNRVSLMCP 110
Db      61 LHVAGAGLELRQMLPRSRPKVLDITGLSTMGC-----LCIANFCGRNRVSLMCP 110
QY      111 SMSPELKOSTCLSLPKCWDYRRAAVRGILEFLLRHRCPTLTQDEYQWCDHSSLQSTPE 170
Db      111 SMSPELKOSTCLSLPKCWDYRRAAVRGILEFLLRHRCPTLTQDEYQWCDHSSLQSTPE 170
QY      111 SMSPELKOSTCLSLPKCWDYRRAAVRGILEFLLRHRCPTLTQDEYQWCDHSSLQSTPE 170
Db      111 SMSPELKOSTCLSLPKCWDYRRAAVRGILEFLLRHRCPTLTQDEYQWCDHSSLQSTPE 170
QY      171 ----IKHRRPASQVAGTKRDMHNHYWMLFIFFLNFRLQSLNSVYQAGVQWQMNLSIQPLP 226
Db      171 SSILLPQP---KVAGTKRDMHNHYWMLFIFFLNFRLQSLNSVYQAGVQWQMNLSIQPLP 226
QY      227 PGFKLFSCPSLLSMDYRRPRPLANFVFLVEMGEF-----TMFAR----LILISGCDLPA 278
Db      227 PGFKLFSCPSLLSMDYRRPRPLANFVFLVEMGEF-----LILISGCDLPA 278
QY      279 SASQASGITGVSHHARLIFNFCLEFMESHSTVYQAGVQWQMNLSLOPLPGLKRFSCSLSP 338
Db      282 --PKVLGQDVTPTARPIFNFCLEFMESHSTVYQAGVQWQMNLSLOPLPGLKRFSCSLSP 339
QY      339 SSMWDGHLRPHRPAHNCIFIRG 360
Db      340 SSMWDGHLHHPPLPFLVFSLG 361

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RESULT 5
US-09-605-785-573
; Sequence 573, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 573
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-605-785-573

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Query Match	12.38;	Score 250;	DB 4;	Length 132;
Best Local Similarity	61.58;	Pred. No. 9.1e-20;		
Matches 48;	Conservative 6;	Mismatches 24;	Indels 0;	Gaps 0;

OY 298 NFFCLFEMSHSVTQAGVQWPNLGSLOPLPPGCIKRRSCSLDSSWDYGILPEHPANFCIFI 357
|| || | ||||| : ||||| : ||||| ||| : ||| |||| -
Db 27 NFFFLRQDSGEVVAQAGVQMHDLSLOPLPHRFKQPSCLSPHSWDHRYAPFHLANFCFS 86
OY 358 RGVSPVLTSGMSQTDLR 375

Db 87 RDGVSLCCGWSKTPGLQ 104

RESULT 6

US-09-058-489-22
Sequence 22, Application US/09058489
Patent No. 6103886

GENERAL INFORMATION:

APPLICANT: Whitehead Institute for Biomedical Research

APPLICANT: Lahn, Bruce

APPLICANT: Page, David

TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
the Y Chromosome

FILE REFERENCE: WI197-08pa

CURRENT FILING DATE: 1998-04-10

EARLIER APPLICATION NUMBER: 60/041,877

EARLIER FILING DATE: 1997-04-11

NUMBER OF SEQ ID NOS: 91

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 22

LENGTH: 1079

TYPE: PRT

ORGANISM: Human

US-09-058-489-22

Query Match 10.7%; Score 218; DB 3; Length 1079;

Best Local Similarity 26.4%; Pred. No. 6.3e-15;

Matches 97; Conservative 30; Mismatches 89; Indels 152; Gaps 16;

QY 25 PGSSDPASASP-----VAGITGM-CTHARLILYFFLVEMEFHVGAG--LELPISD 74
DB 766 PSAATSTPSPKSTEGKINSVSLNSPHGL-----HTVNGEGKGSOSTKVDPLAS 821
QY 75 D-----PSVASASOANRYRGHARLCLANPCGNRVSLMCPSPSPK----- 117
DB 822 HRSTSQLPMSVS-----ICPSTEVLLKCRNPGKNGL 855
QY 118 QSTCLSKCWDYRAAIVGLFLFLRHRCPTLLQDEVQMDHSLSPSPET----- 171
DB 856 SNSCLLDKCPRPRTSP-----YPLPKDK-----LMPPTSTYLENKR 896
QY 172 -----KHP-----PAS 177
DB 897 DAFPPPLHQPCTNPVTVIRGLAGALKLDLGLSTKLVEANNEHWEVRYTOLLQPAD 956
QY 178 AS-QVAGTK-----DMHHTWLIFFIFNFKRQSLNSVYQAGYQMRNLSLQPLPGF 229
DB 957 ENMDPTGKKIWRCEHSNRSHTTIAYK--OYQASSFQESLRAGMOWCDLSLQPPPGF 1013
QY 230 KLFSPCLSSWDYRRPRLANFVFLVEMGFTMFARL--ILISGPCDLPASASOSAGI 286
DB 1014 KRSHLSLPSNMNVRHLPSCPTNRCIFVETGFGHVGACLELITSG--GLASASOSAGI 1071
QY 287 TGVSHHAR 294
DB 1072 TGVSHHAR 1079

RESULT 7

US-09-227-357-193

Sequence 193, Application US/09227357
Patent No. 6342581

GENERAL INFORMATION:

APPLICANT: Fischer et al.

TITLE OF INVENTION: 123 Human Secreted Proteins

FILE REFERENCE: P2010P1

CURRENT FILING DATE: 1999-01-08

EARLIER APPLICATION NUMBER: PCT/US98/13684

EARLIER FILING DATE: 1998-07-07

EARLIER APPLICATION NUMBER: 60/051,926

OTHER INFORMATION: Xaa equals stop translation

EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
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EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 193
LENGTH: 110
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (110)
OTHER INFORMATION: Xaa equals stop translation


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RESULT 10
US-09-227-357-285
; Sequence 285, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,932
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
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; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
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; EARLIER FILING DATE: 1997-08-18
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; EARLIER FILING DATE: 1997-08-18
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; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12

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; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 285
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-285

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Query Match
Best Local Similarity 70.7%; Score 158; DB 4; Length 122;
Matches 29; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

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QY 322 LQPLPGIKRSCSLSSNDYGLPHRPAFCIFRIGVGS 362
DB 1 MQALPGFKPSCSLSPSRWDYGCATQHPANFCIFRDRVS 41

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RESULT 11
US-09-265-630-11
; Sequence 11, Application US/09265630
; Patent No. 6432814
; GENERAL INFORMATION:
; APPLICANT: LEVINE, BETH C
; TITLE OF INVENTION: BECLIN AND USES THEREOF
; FILE REFERENCE: 50902-D/JPM/EMW
; CURRENT APPLICATION NUMBER: US/09/265,630
; CURRENT FILING DATE: 1999-03-09
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 11
; LENGTH: 388
; TYPE: PRT
; ORGANISM: human
US-09-265-630-11

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Query Match
Best Local Similarity 65.1%; Score 155; DB 4; Length 388;
Matches 28; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

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QY 310 TQAGVQWPNLGSLOPLPGIKRSCSLSPSRWDYGLPHRPA 352
DB 346 SKAEVQWHLGLQPPRPFQKPFCLSLSTWDYHAPRPA 388

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RESULT 12
US-09-227-357-171
; Sequence 171, Application US/09227357
; Patent No. 6342581
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/227,357
; CURRENT FILING DATE: 1999-01-08
; EARLIER APPLICATION NUMBER: PCT/US98/13684
; EARLIER FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: 60/051,926
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,793
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,925
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,929
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,803
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,732
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,931

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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
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EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
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EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
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EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 171
LENGTH: 90
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (90)
OTHER INFORMATION: Xaa equals stop translation
US-09-227-357-171

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Query Match
Best Local Similarity 6.9%; Score 141; DB 4; Length 90;
Matches 44; Conservative 13; Mismatches 26; Indels 42; Gaps 6;

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QY 46 HARLLVFEVMEFLHVGQAGLEPTSDPSVSASOSARVYTG--HHARLCLANFCGRN 103
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 3 HVAWLIFFVLEMGCHVGQAGLKLTLSDPPASASOSAGI--TGVSHNA-----WGR 54
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 104 RVSLMCPSPLELKSTCLSLPKCWDYRAAVPGILFFLRHRCPTLTODEVQWCDH-- 161
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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DB 55 YFQNIWNNSPPKPRQ-----GLILL-----PRLMOGHHR 84
QY 162 SSTLP 166
| : : : : : |
DB 85 SSTLP 89

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RESULT 13
US-09-288-143-168
Sequence 168, Application US/09288143
Patent No. 6433139
GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: P2018P1
CURRENT APPLICATION NUMBER: US/09/288,143
EARLIER FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
EARLIER FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,463
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 219
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 168
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-09-288-143-168

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Query Match
Best Local Similarity 6.4%; Score 129.5; DB 4; Length 99;
Matches 46; Conservative 13; Mismatches 29; Indels 99; Gaps 6;

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QY 107 LMCPSPLELKSTCLSLPKCWDYRAAVPGILFFLRHRCPTLTODEVQWCDHSLP 166
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DB 1 LCCPGHS-----AVRSM-----LTATLASVQALIMP- 28
QY 167 STPEIKHPASASQVAGTKDMHHTWLFIFIFNPLROSINSVYQAGVQWRNLGSLQPLP 226
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 29 -----SASQVAGITSVHHQQLSFVL--VEMGLCHVGQGLK----- 64
QY 227 PGFKLFSCPSLLSSNDYRRPRPLANFVLEMGFTMFARLLIISPCCLPASASOSAGI 286
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DB 65 -----LLAS-----SOLPASASOSAGI 81
QY 287 TGVSHHA 293
| : : : : : |
DB 82 TGVSHHS 88

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```

RESULT 14
US-08-951-200A-1
Sequence 1, Application US/08951200A
Patent No. 6013495
GENERAL INFORMATION:
APPLICANT: Schwartz, Martin A.
APPLICANT: Meredith Jr., Jere E.
APPLICANT: Takada, Yoshikazu
APPLICANT: Langino, Lucia
TITLE OF INVENTION: METHODS OF USE FOR INTEGRIN BLC CELL
GROWTH INHIBITOR
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,200A
FILING DATE: 14-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,118
FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/026002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-951-200A-1

Query Match
Best Local Similarity 6.3%; Score 128; DB 3; Length 48;
Matches 24; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 306 SHSVTQAGVQWPNLGSLOPLPPGLKRFSCSLPSSMDY 343
1 SLSVAQPGVQWCHISLOPLTSPRFGQFSCSLPSTWDY 38
Db

RESULT 15
US-08-951-200A-8
Sequence 8, Application US/08951200A
Patent No. 6013495
GENERAL INFORMATION:
APPLICANT: Schwartz, Martin A.
APPLICANT: Meredith Jr., Jere E.
APPLICANT: Takada, Yoshikazu
APPLICANT: Languiño, Lucia
TITLE OF INVENTION: METHODS OF USE FOR INTEGRIN BIC CELL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,200A
FILING DATE: 14-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,118

FILING DATE: 21-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07300/026002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFAX: (619) 678-5099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-951-200A-8

Query Match
Best Local Similarity 6.0%; Score 122; DB 3; Length 53;
Matches 23; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 306 SHSVTQAGVQWPNLGSLOPLPPGLKRFSCSLPSSMDY 343
1 SLSVAQPGVQWCHISLOPLTSPRFGQFSCSLPSTWDY 43
Db

Search completed: July 17, 2003, 18:20:42
Job time : 28 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 17, 2003, 18:07:23 ; Search time 72 Seconds
(without alignments)
694.014 Million cell updates/sec

Title: US-09-380-203-2
Perfect score: 2034
Sequence: 1 MEFSLPLRLCEKNGAISNR.....FIRGVSPYLSGWSQTPLDR 375

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	100.0	375	21 AAB01399	Neuron-associated
2	2034	100.0	375	23 ABB81538	Neural thread prot
3	1415.5	69.6	397	17 AAR95913	Neural thread prot
4	928	45.6	381	22 AAU30235	Novel human secret
5	927.5	45.6	382	22 AAU31818	Novel human secret
6	927.5	45.6	382	22 AAU32610	Novel human secret
7	927.5	45.6	382	22 AAU32707	Novel human secret
8	849	41.7	324	22 AAU28573	Novel human secret
9	849	41.7	324	22 AAU28579	Novel human secret
10	822.5	40.4	411	22 ABG08428	Novel human diagno

11	739	36.3	317	22 AAU33200	Novel human secret
12	735	36.1	290	22 ABG21913	Novel human diagno
13	734.5	36.1	361	22 ABG68738	Human prostate spe
14	609	29.9	257	22 AA010294	Human polypeptide
15	590	29.0	276	22 ABG07919	Novel human diagno
16	574	28.2	185	22 AA006014	Human polypeptide
17	569	28.0	241	22 ABBI1464	Human neuronal thr
18	563	27.7	202	22 AAU30686	Novel human secret
19	561	27.6	250	22 AAU31823	Novel human secret
20	560	27.5	296	22 AAU33304	Novel human secret
21	553	27.2	175	22 AAU31782	Novel human secret
22	550.5	27.1	215	22 AAU31513	Novel human diagno
23	546	26.8	215	22 ABG07921	Novel human diagno
24	543.5	26.7	216	22 AAU32615	Novel human secret
25	524	25.8	304	22 AAU30391	Novel human secret
26	522.5	25.7	175	22 AAU31857	Novel human secret
27	521.5	25.6	418	22 AAU31980	Novel human secret
28	520	25.6	396	22 AAU30455	Novel human secret
29	517	25.4	213	22 AAU25396	Human protein sequ
30	504.5	24.8	196	22 AAU31786	Novel human secret
31	503	24.7	189	22 AAU31834	Novel human secret
32	500.5	24.6	222	22 AAU31887	Novel human secret
33	496	24.4	229	22 AAU30354	Novel human secret
34	495.5	24.4	213	22 AAU31789	Novel human secret
35	488.5	24.0	293	22 AAU31676	Novel human secret
36	484.5	23.8	378	22 AA012915	Human polypeptide
37	482	23.7	85	21 AAB28760	Peptide #5. Homo
38	475	23.4	228	22 AA012783	Human polypeptide
39	471.5	23.2	210	22 AAU31810	Novel human secret
40	471	23.2	286	22 AAU28297	Novel human secret
41	464	22.8	154	22 ABG08425	Novel human diagno
42	461	22.7	293	22 AAU31668	Human bone marrow
43	457.5	22.5	264	22 ABG22078	Novel human diagno
44	457.5	22.5	264	22 ABG22078	Novel human secret
45	447	22.0	84	21 AAB51458	Human secreted pro

ALIGNMENTS

RESULT 1	
AAB01399	
ID	AAB01399 standard; Protein; 375 AA.
XX	
AC	AAB01399;
XX	
DF	20-OCT-2000 (first entry)
DE	
XX	Neuron-associated protein.
XX	
KW	Neuron associated protein; NEUP; neurological disorder; epilepsy;
KW	ischemic cerebrovascular disease; stroke; cerebral neoplasm;
KW	Alzheimer's disease; Pick's disease; Huntington's disease;
KW	dementia; Parkinson's disease; demyelinating disease; meningitis;
KW	prion disease; kuru; Creutzfeldt-Jakob disease; neurofibromatosis;
KW	cerebral palsy; muscular dystrophy; central nervous system; CNS;
KW	peripheral nervous system; PNS; myopathy; schizophrenia;
KW	actinic keratosis; arteriosclerosis; atherosclerosis; bursitis;
KW	cirrhosis; hepatitis; mixed connective tissue disease; MCTD;
KW	myelofibrosis; paroxysmal nocturnal haemoglobinuria; cancer;
KW	autoimmune disease; inflammation; acquired immunodeficiency syndrome;
KW	AIDS; Addison's disease; adult respiratory distress syndrome;
KW	allergy; ankylosing spondylitis; amyloidosis; anaemia; asthma;
KW	Werner syndrome; trauma; human.
OS	Homo sapiens.
XX	
PN	WO200034477-A2.
XX	
PD	15-JUN-2000.
XX	
PF	10-DEC-1999; 99WO-US30408.
XX	

PR 11-DEC-1998; 9805-0210083.
PR 11-DEC-1998; 9805-9123456.
PR 09-FEB-1999; 9905-0119365.
PR 16-MAR-1999; 9905-0124687.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YF, Yue H, Baughn MR, Hillman JL, Lal P, Au-young J, Yang J;
PI Lu DM, Azimzal Y;
DR WPI: 2000-423423/36.
XX
PT New human neuron-associated proteins and polynucleotides encoding them,
PT useful for diagnosis, treatment and prevention of cell proliferative
PT disorders including cancer, neuronal and neurological disorders
XX
PS Disclosure; Page 143-144; 145pp; English.
XX
CC Human neuron-associated proteins (NEUAP) can be used for
CC treating or preventing a disorder associated with decreased
CC expression or activity of NEUAP. Antagonists of NEUAP are useful for
CC treating or preventing disorder associated with increased expression
CC or activity of NEUAP. NEUAP or their fragments or derivatives are
CC useful for treating neurological disorder such as epilepsy, ischemic
CC cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's
CC disease, Pick's disease, Huntington's disease, dementia and
CC Parkinson's disease. NEUAPs are also useful for treating other
CC demyelinating diseases, bacterial and viral meningitis, prion
CC diseases including kuru, Creutzfeldt-Jakob disease, nutritional and
CC metabolic diseases of the nervous system, neurofibromatosis, other
CC developmental disorders of the central nervous system, cerebral
CC palsy, neuromuscular disorders, autonomic nervous system disorders,
CC cranial nerve disorders, spinal cord diseases, muscular dystrophies and
CC other neuromuscular disorders, peripheral nervous system disorders,
CC inherited, metabolic, endocrine, and toxic myopathies, mental
CC disorders, including mood, anxiety and schizophrenic disorders, a cell
CC proliferative disorder such as actinic keratosis, arteriosclerosis,
CC atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective
CC tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal
CC haemoglobinuria, cancers of the adrenal gland, bladder, bone,
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's
CC disease, adult respiratory distress syndrome, allergies, ankylosing
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,
CC complications of cancer, hemodialysis, and extracorporeal circulation,
CC viral, bacterial, fungal parasitic, protozoal, and helminthic
CC infections, and trauma. This protein was designated g3002527.
XX
SO Sequence 375 AA:
Query Match 100.0%; Score 2034; DB 21; Length 375;
Best Local Similarity 100.0%; Pred. No. 2,1e-198;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLEPRLCNCALSAHNRNLPPSSSDPASASPVAGTGMCTHARLLIYFLEVMEEF 60
DB 1 MEFSLLEPRLCNCALSAHNRNLPPSSSDPASASPVAGTGMCTHARLLIYFLEVMEEF 60
QY 61 LHWGAGLELPTSDPVSASOSARXRTGHHARLLCNAFCGRNVNLSMCSWSPKOST 120
DB 61 LHWGAGLELPTSDPVSASOSARXRTGHHARLLCNAFCGRNVNLSMCSWSPKOST 120
QY 61 LHWGAGLELPTSDPVSASOSARXRTGHHARLLCNAFCGRNVNLSMCSWSPKOST 120
DB 61 LHWGAGLELPTSDPVSASOSARXRTGHHARLLCNAFCGRNVNLSMCSWSPKOST 120
QY 121 CUSLPKCDYRAAVPCLFLTLFLRHRCPTLTQDEVQWCHSSLOPSTPEIKHPASASQ 180
DB 121 CUSLPKCDYRAAVPCLFLTLFLRHRCPTLTQDEVQWCHSSLOPSTPEIKHPASASQ 180
QY 121 CUSLPKCDYRAAVPCLFLTLFLRHRCPTLTQDEVQWCHSSLOPSTPEIKHPASASQ 180
DB 121 CUSLPKCDYRAAVPCLFLTLFLRHRCPTLTQDEVQWCHSSLOPSTPEIKHPASASQ 180
QY 181 VAGTKDMHRYTWLFIFFLNFLOSINVTQAGVQWRNLGSIQPLPGFLLFCSPILSS 240
DB 181 VAGTKDMHRYTWLFIFFLNFLOSINVTQAGVQWRNLGSIQPLPGFLLFCSPILSS 240
QY 241 WQYRPPRLANFVFLVEMGTFMFARLILISGCDLPASASOSAGITGVSHARLLIFNFC 300
DB 241 WQYRPPRLANFVFLVEMGTFMFARLILISGCDLPASASOSAGITGVSHARLLIFNFC 300

QY 301 LPEMESHVTOAGVQWNLGSLQPLPGIKRRESCLSPSSNDVGHCLPPHPANCFIRGC 360
DB 301 LPEMESHVTOAGVQWNLGSLQPLPGIKRRESCLSPSSNDVGHCLPPHPANCFIRGC 360
QY 361 VSPYLSGWSQTPDLR 375
DB 361 VSPYLSGWSQTPDLR 375
RESULT 2
ID ABB81538 standard; Protein: 375 AA.
XX ABB81538;
XX
XX 02-SEP-2002 (first entry)
DE Neural thread protein (NTP).
XX
XX Neural thread protein; NTP, Harill peptide; Alzheimer's disease;
KW Down's syndrome; neuroectodermal tumour; astrocytoma; glioblastoma;
KW hypoxia; ischaemia; cerebral infarction.
XX
XX Homo sapiens.
XX
XX MO200234915-A2.
XX
XX 02-MAY-2002.
XX
XX 25-OCT-2001; 2001MO-US42813.
XX
XX 27-OCT-2000; 2000US-0697590.
XX
XX (NIMO-) NYMOX PHARM CORP.
XX
XX Fitzpatrick J, Averbach P, Focht MSS, Blbiano R;
XX
XX WPI: 2002-507998/54.
XX
XX N-FSDB; ABB89470.
XX
XX
XX New Harill peptide sequences of the Neural Thread Protein, useful in
XX therapeutic assays, e.g. as targets for developing drugs for treating
XX Alzheimer's disease, ischemia or cerebral infarction, or for diagnosing
XX these diseases -
XX
XX Example 1; Fig 1; 53pp; English.
XX
XX The present invention describes a neural thread protein (NTP) peptide
XX having an amino acid sequence selected from ABB81511 to ABB81529 and
XX their homologues, which are referred collectively as Harill peptides (1).
XX (1) have neuroprotective, nootropic, vasotropic and cerebroprotective
XX activities, and can be used in peptide therapy. The Harill peptide
XX sequences can be used as analogues for NTP in therapeutic or diagnostic
XX assays by replacing NTP with the peptide in such an assay. The Harill
XX peptides are also useful as a trap material in a diagnostic or
XX therapeutic assay. Therefore, the Harill peptides are useful in binding
XX assays, protein and antibody purification, therapeutics or diagnostics.
XX In particular, the peptides are also useful for diagnosing Alzheimer's
XX disease, Down's syndrome, neuroectodermal tumours, astrocytomas,
XX glioblastomas, hypoxia, ischaemia or cerebral infarction. The peptides
XX are also useful as targets for drug development for the treatment of
XX these diseases. The present sequence represents a neural thread protein
XX given in the exemplification of the present invention.
XX
SO Sequence 375 AA:
Query Match 100.0%; Score 2034; DB 23; Length 375;
Best Local Similarity 100.0%; Pred. No. 2,1e-198;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEFSLLEPRLCNCALSAHNRNLPPSSSDPASASPVAGTGMCTHARLLIYFLEVMEEF 60
DB 1 MEFSLLEPRLCNCALSAHNRNLPPSSSDPASASPVAGTGMCTHARLLIYFLEVMEEF 60

Db 1 MESSLLPRLKCNCAISAHNRRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
 QY 61 LHWGAGLELPTSDPVSASOSARVYRTGHHARLCLANFCGRNVSLMCPMSPELKOST 120
 Db 61 LHWGAGLELPTSDPVSASOSARVYRTGHHARLCLANFCGRNVSLMCPMSPELKOST 120
 QY 121 CLSLPKCMQDYRAAVPGLFLIFLFRHRCPTLTODEVOMCHSSIQPSTPEIKHPASASQ 180
 Db 121 CLSLPKCMQDYRAAVPGLFLIFLFRHRCPTLTODEVOMCHSSIQPSTPEIKHPASASQ 180
 QY 181 VASTKDMHNTWLIFFIFENFLRQSLNSVYQAGVOMNLSLOPLPPGFKLFSCPSLSS 240
 Db 181 VASTKDMHNTWLIFFIFENFLRQSLNSVYQAGVOMNLSLOPLPPGFKLFSCPSLSS 240
 QY 241 WDTRRRPRLANFVFLVEMGFTMFARLLISGPCDLLPASASOSAGITGVSHHARLIFNFC 300
 Db 241 WDTRRRPRLANFVFLVEMGFTMFARLLISGPCDLLPASASOSAGITGVSHHARLIFNFC 300
 QY 301 LFEMESHVYQAGVOMNLSLOPLPPGLKRFSCSLSPSSMDYGHLPPHPANFCIFIRGG 360
 Db 301 LFEMESHVYQAGVOMNLSLOPLPPGLKRFSCSLSPSSMDYGHLPPHPANFCIFIRGG 360
 QY 361 VSPYLSGMSQTPDLR 375
 Db 361 VSPYLSGMSQTPDLR 375

RESULT 3
 AAR95913 standard; Protein: 397 AA.
 ID AAR95913
 AC AAR95913;
 XX
 DF 13-NOV-1996 (first entry)
 DE Neural thread protein.
 XX
 KW Neural thread protein; NTP; diagnosis; detection;
 KM Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;
 KM monoclonal antibody; binding fragment.
 OS Homo sapiens.
 XX
 PN WO9615272-A1.
 XX
 PD 23-MAY-1996.
 XX
 PF 14-NOV-1995; 95MO-US17111.
 XX
 PR 14-NOV-1994; 94US-0340426.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PI De LA MONTE S, Wands JR;
 XX
 DR N-PSDB; AAT27738.
 XX
 DR N-PSDB; AAT27738.
 XX
 PT Detection of neural thread protein in diagnosis of Alzheimer's
 PT disease - also NTP DNA and protein sequences used in gene and
 PT anti-sense therapy
 XX
 PS Claim 22; Page 171-172; 238pp; English.
 XX
 CC A method for detecting the presence of neural thread protein (NTP)
 CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human
 CC subject comprises (a) contacting a sample from a human subject that
 CC is suspected of containing the NTP with at least one molecule
 CC capable of binding to the protein; and (b) detecting any of the
 CC molecule bound to the protein. The binding molecule is selected
 CC from an antibody free of natural impurities, a monoclonal antibody
 CC or a binding fragment of either of these. The method may be used for
 CC diagnosing the presence of Alzheimer's disease, neuroectodermal

CC tumours and a malignant astrocytoma in a human.
 XX
 SQ Sequence 397 AA:
 Query Match 69.6%; Score 1415.5; DB 17; Length 397;
 Best Local Similarity 74.6%; Pred. No. 2.2e-135;
 Matches 285; Conservative 10; Mismatches 44; Indels 43; Gaps 7;

QY 1 MESSLLPRLKCNCAISAHNRRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
 Db 1 MESSLLPRLKCNCAISAHNRRLRPGSSDSPASAPVAGITGMCTHARLLIYFLVEMEF 60
 QY 61 LHWGAGLELPTSDPVSASOSARVYRTGHHARLCLANFCGRNVSLMCPMSPELKOST 110
 Db 61 LHWGAGLELPTSDPVSASOSARVYRTGHHARLCLANFCGRNVSLMCPMSPELKOST 110
 QY 111 SMSPELKOSTCLSLPKCMQDYRAAVPGLFLIFLFRHRCPTLTODEVOMCHSSIQPSTPE 170
 Db 111 SMSPELKOSTCLSLPKCMQDYRAAVPGLFLIFLFRHRCPTLTODEVOMCHSSIQPSTPE 170
 QY 171 ----IKHPPASASQVAGTKDMHNTWLIFFIFENFLRQSLNSVYQAGVOMNLSLOPLP 226
 Db 171 SSIILPQP-----KVAGTKDMHNTWLIFFIFENFLRQSLNSVYQAGVOMNLSLOPLP 226
 QY 227 PGFKLFSCPSLSSMDYRRPPRLANFVFLVEMGFTMFAR-----LILISGPCDLPA 278
 Db 227 PGFKLFSCPSLSSMDYRRPPRLANFVFLVEMGFTMFAR-----LILISGPCDLPA 278
 QY 279 SASOSAGITGVSHHARLIFNFCLEFEMESHVYQAGVOMNLSLOPLPPGLKRFSCSLSP 338
 Db 282 --PKVLGLQDVTPPARPIFNFCLEFEMESHVYQAGVOMNLSLOPLPPGLKRFSCSLSP 339
 QY 339 SSMWYGHLPHPANFCIFIRGG 360
 Db 340 SSMWYGHLPHPANFCIFIRGG 361

RESULT 4
 AAU30235 standard; Protein: 381 AA.
 ID AAU30235
 AC AAU30235;
 XX
 DT 18-DEC-2001 (first entry)
 DE Novel human secreted protein #726.
 XX
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 XX
 PN WO200179449-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 16-APR-2001; 2001WO-US08656.
 XX
 PR 18-APR-2000; 2000US-0552929.
 XX
 PR 26-JAN-2001; 2001US-0770160.
 XX
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI; 2001-611725/70.
 XX
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 XX
 PS Claim 20; Page 264-265; 765pp; English.
 XX

The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; to suppress and/or stimulate; as anti-inflammatory agents; and in treatment of leukemias. AM29510-AM93304 represent the amino acid sequences of novel human secreted proteins of the invention.

5Q	Sequence	381 AA
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Query Match	45.68;	Score 928;	DB 22;	Length 381;
Best Local Similarity	55.98;	Pred. No. 8.8e-86;		
Matches 223;	Conservative 27;	Mismatches 101;	Indels 48;	Gaps 14;

```

OY 4 SLILPRLCEGALSHARNILCPGSSDSPAASVAITOMCHALIFELVEMELFY 63
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 4 SLILPRLCEGALSHARNILCPGSSDSPAASVAITOMCHALIFELVEMELFY 62
OY 64 GOALLETPTDPSVASASARVYTG--HHARCLANPCGRNRYSLMCPM----- 112
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 AQAGLEILYDSTYL-ASOSAGI-TGVNHHALMF--FCSRDYVSLCPGSKRYAKSRIT 118
OY 113 --SPELKOSTCJSLPCMDYRPAAN-PGLFIFELRHRCPLTODEYQWCDHSSLQ-- 166
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 ATISGLKXFCASELPSRDRYHVRPHNGNCIP-----GRDEVSPC-----WPGF 164
OY 167 STEPIKRPASASOVAGTFKQMHNYT---LIFIFLNFRLQSLNSVQAGVQWRNLGSL 222
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 165 XTDLPRAPRASASQSAEILIGVSHHTWQVEFLNLNFIYLRNSLSDVAQARVQRDUGSL 224
OY 223 QPLPFGKFLCSPCSLSLSDYR--PRLIANFEVLEVMGFTWAFARLLISQPCDLPASAS 281
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 225 QAPPRKRPSCSLSPSSWDYRPPRPAPNPFELVETGTFYLARVYLISKPRDLPASAS 284
OY 282 QSAQITGVSHHAILFNFCLFEMESHESHTVAGQVNPMLISLOLPRLPGIKRFSCSLSPSSM 341
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 285 QSAQITGVSHHRLTIFNF--FETGSHVTAAWQVYTISLQPRRLKXSHHLLITSNW 342
OY 342 DYGLHPHPAN-----FCLFLRGVSVYSLSGMSQTDRLR 375
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 343 DYRCTPPCPNLFYILFYIFHRDGLSLCCGMSKXTPEIK 381

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	RESULT 5
XX	AAU31818
ID	AAU31818 standard; Protein; 382 AA.
XX	
AC	AAU31818;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Novel human secreted protein #2309.
XX	
KW	Human; vaccination; gene therapy; nutritional supplement;
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW	immune suppression; immune stimulation; anti-inflammatory; leukaemia
OS	Homo sapiens.
XX	
PN	WO200179449-A2.
XX	
PD	25-OCT-2001.
XX	

PE 16-APR-2001; 2001WO-US086556.
XX
PR 18-APR-2000; 2000US-0552929.
PR 26-JAN-2001; 2001US-0770160.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dymnace RT;
XX
DR WPI; 2001-611725/70.
XX
PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX vaccination, testing and therapy -
XX
ES Claim 20; Page 513; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, feeding and
CC therapy and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation, to regulate hematopoiesis, and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AA023510-AA031304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.

SQ Sequence 382 AA;

Query Match	45.68;	Score 927.5;	DB 22;	Length 382;
Best Local Similarity	55.88;	Pred. No. 1e-85;		
Matches 223; Conservative	27;	Mismatches 101;	Indels 49;	Gaps 14;

```

OY      4 SLLPRLPENCALSAHNRLRIGSSSPSPASPAVAGTIGCTARILFELFVLEWEPFLAV 63
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 SLLPRLPENCALIAHNCNLSSSDSPASASOYTGTIGCTHITOLL FVFLVEMGFNHTI 62

OY      64 GAGIELPTSDPESVASASGARITRG--HARCLANFCGRNYSIMCPSMS----- 113
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      63 AAGAGELTTSPTL-ASQAGI-TGVNHNHMLFF--FCSRDVYSJCYGWSRVAAXSHIT 118
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      114 ----PELKOSTCSLPKCMWYRRAAV-EGELELFELRHRCPITLDEYOWCMHSDIOP-- 166
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      119 ATSAAGELKXFCFSLPESRDYRHVPRPHGNCIF-----GREYVSPC-----WPGW 164

OY      167 -STPEIKRPPASASOVAGTGRDMHNHTW----LIFIFPNFLROSLYASQACVQWRNIGS 221
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      165 KETPRLKRPASASQSNELIGVSHHTWQOYFELFNLFIYLRMSLDSVAQAIVQORLUGS 224
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      222 LQPLRPGKLFSCPSGLLSDMDYR-PRLANFEVLYEMGFYFARLLIISGCDLPASA 280
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      225 LQAPRPKRPKPSCLSDSSWDYRRPRPHANFEVLETFYIARVYLIXSPRLDPSA 284
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY      281 SOSAGITGVSHHALLFNFCLFEMESHVSTAGVQANGLSLOPLRPGKFRSCSLSPSS 340
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      285 SOSAGITGVSHHTRLFNF--FETGSHVTAIVQWITISLOPLRPRPELKSXSHLITSN 342

OY      341 WDYGHLRPHRAN-----FCFLIRGVSPYLSGWSQOTDRLR 375
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      343 WDYRCPRPENFLFYLFYFNHSDQSLCCGWSXTEPK 382

```

RESULT 6
AAU32610
ID AAU32610 standard; Protein; 382 AA
XX

[illegible]

Dd	225	LQAPPRKRPSCLSLSSMDRRPPHPANFVLVEGFTVLAARRVLTSPRDLPA	284
Oy	281	SQSAGITGVSHHARLIINFNCLEFMESHSTYAGVOMPNIGSLQPLPGCKRFSCSLPSS	340
Dd	285	SOSAGITGVSHHTRILFINF--FETHTHSVTMAAAVMYTIGSLQPRTPELKXSHLLITSN	342
Oy	341	WDYGHLPPHPAN----FCIFIRGVSPFLSGWSCPDPDR	375
Dd	343	WDYRCTPCPPNLFIYLFIFYFHREDGSLCCPGMSXYTEPK	382
RESULT 7			
ID	AAU32707	standard: Protein; 382 AA.	
XX	AAU32707;		
AC			
XX	AAU32707;		
DT	18-DEC-2001	(first entry)	
XX			
DE	Novel human secreted protein #3198.		
KW	Human; vaccination; gene therapy; nutritional supplement;		
KW	stem cell proliferation; haematopoiesis; nerve tissue regeneration;		
XX	immune suppression; immune stimulation; anti-inflammatory; leukaemia.		
XX	Homo sapiens.		
XX	WO200179449-A2.		
PN			
PD	25-OCT-2001.		
PF	16-APR-2001; 2001WO-US08656.		
XX			
PR	18-APR-2000; 2000US-0552929.		
PR	26-JAN-2001; 2001US-0770160.		
XX			
PA	(HYSE-) HYSEQ INC.		
PI	Tang YF, Liu C, Drmanac RT;		
DR	WPI: 2001-611725/70.		
PT	Nucleic acids encoding a range of human polypeptides, useful in genetic		
XX	vaccination, testing and therapy -		
PS	Claim 20; Page 652; 765pp; English.		
XX			
CC	The invention relates to novel human secreted polypeptides. The		
CC	polypeptides and antibodies to the polypeptides are useful for		
CC	determining the presence of or predisposition to a disease associated		
CC	with altered levels of polypeptide. The polypeptides are also useful for		
CC	identifying agents (agonists and antagonists) that bind to them. Cells		
CC	expressing the proteins are useful for identifying a therapeutic agent		
CC	for use in treatment of a pathology related to aberrant expression or		
CC	physiological interactions of the polypeptide. Vectors comprising		
CC	the nucleic acids encoding the polypeptides and cells genetically		
CC	engineered to express them are also useful for producing the proteins.		
CC	The proteins are useful in genetic vaccination, testing and		
CC	therapy, and can be used as nutritional supplements. They may be used to		
CC	increase stem cell proliferation; to regulate haematopoiesis; and in		
CC	bone, cartilage, tendon and/or nerve tissue growth or regeneration;		
CC	immune suppression and/or stimulation; as anti-inflammatory agents; and		
CC	in treatment of leukaemias. AAU329510-AAU33304 represent the amino acid		
CC	sequences of novel human secreted proteins of the invention.		
XX			
SQ	Sequence 382 AA;		
Query Match	45.6%;	Score 927.5;	DB 22; Length 382;
Best Local Similarity	55.8%;	Pred. No. Ie-85;	
Matches 223; Conservative	27;	Mismatches 101;	Indels 49; Gaps 14
OY	4 SLLPRLCEGNCAISHRNRI.LPGSSDPSASPVAGINGMCTHARLI.YFFLVEMDFLHV	63	

DR WPI: 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
XX
XX
PS Claim 20; Page 168; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon, and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukaemias. AA029510-AA03304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX
SQ Sequence 324 AA:
Query Match 41.7%; Score 849; DB 22; Length 324;
Best Local Similarity 50.8%; Pred. No. 7,8e-78;
Matches 200; Conservative 10; Mismatches 62; Indels 122; Gaps 10;
OY 1 MEFSLLPRLCNGAISAHRNRLPGSSDPSASPVAGITGCTHARLILYFLVEMEF 60
DB 34 MEFSLLPRLCNGAISAHRNRLPGSSDPSASPVAGITGCTHARLILYFLVEMEF 92
OY 61 LHVGAAGLELPTSDPSVSASOSARYRIGHARLCLANFCGRNRVSLMCPSPSELKOST 120
DB 93 HHVGAAGLELPTSDPSVSASOSARYRIGHARLCLANFCGRNRVSLMCPSPSELKOST 109
OY 121 CLSLKCMQDYR-AAVPGLEFLFRLHRCPTLTODEVQCHDSLQSPTEIKHPPASAS 179
DB 110 CGLRCPMDYRKAATAPGLE-----T 129
OY 180 QVAGTKDMHNYTLIFIFLNFRLQSLNSVTQAGVQMRNLSLQ-PLPPGFLESCPSLL 238
DB 130 -----FFFLRQSFILVAGAGVQMRNLSLQPPRRFRQFSLSLP 170
OY 239 S---SMDYR-PPRLAN-----FVFLVEMGFTMFARLILISGP--CDLPASASQAGIT 287
DB 171 STMSVYRRAAPCPANFVFFFEFLVEKGFSSMLRLVLSXPHDPPRPAASQAGIT 230
OY 288 GSHHAR-----LIFNCLFEMESHVYQAGVQMRNLSLQPLPGKLRFCISLPSW 341
DB 231 GVSHHTRPMSFNITFFFEFFETESVAQAGVQMRNLSLQPPRRFRQFSLSLSSW 290
OY 342 DYGHLPHPANCFIRGVSPLYSGWSQTPDLR 375
DB 291 DYRVPMPMGXCFIRROGVSPRMSGWSOTPDLK 324
RESULT 10
ABC08428
ID ABC08428 standard; Protein; 411 AA.
XX
XX ABC08428;
AC
XX
XX 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #8419.
DE
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX

OS Homo sapiens.
XX
XX W0200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
DR N-PSDB; AAS72615.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20: SEQ ID No 38787; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 411 AA:
Query Match 40.4%; Score 822.5; DB 22; Length 411;
Best Local Similarity 51.0%; Pred. No. 5,4e-75;
Matches 200; Conservative 37; Mismatches 120; Indels 35; Gaps 14;
OY 4 SLLPRLCNGAISAHRNRLPGSSDPSASPVAGITGCTHARLILYFLVEMEF 63
DB 12 SLLPRLCNGAISAHRNRLPGSSDPSASPVAGITGCTHARLILYFLVEMEF 70
OY 64 GQAGLELPTSDPSVSASOSAR-YRIGHAR--LCLANFCGRNRVSLMCPSPSELKOST 120
DB 71 GQAGLELPTSDPSVSASOSAR-YRIGHAR--LCLANFCGRNRVSLMCPSPSELKOST 127
OY 121 CLS-----LPKCMQDYRRAAVPGLEFLFRLHRCPTLTODEVQCHDSLQSPTEIK 172
DB 128 FFSQDSXKSSRYPK-----KLGMVYAIINIGRTYKXKFKETREYIGH-SIHRN 179
OY 173 HPPASASQVAGTKDMHNYTLI---FIFLNFRLQSLNSVTQAGVQMRNLSLQPLPGCF 229
DB 180 H-GVNTYHVAASEK-LHYTYRBMKKAKNFFFLRLRELASVAQAGVQMRNLSLQPPPGF 237
OY 230 KLFPSPSLSSMDYR--PPRLANFVFLVEM--GFTMFARLILISGPDLPASASQAG 285
DB 238 TPFSCPASLRSDYRVRVLPCLANFELYFSMRGRTYFSRMVYSISKPDOPASASQAG 297

OY 286 ITGVSHARTL--IFNFCLE-EMESHVTOAGVOMPLUGSLOPLPRGLKRFSCSLSPSSWD 342
 DB 298 ITGVSHARTLKIIFFFFESETESRVAOAGVOMHDLGSRHRPPGFTFFSCSLSPSSWD 357
 OY 343 YGHLPPHPANPCIFIRGCVSPYLSGMSQTPDL 374
 DB 358 YRGPPRPNANPCVFSRDGVSPOXGWSRSPDL 389
 RESULT 11
 ID AU33200 standard; Protein; 317 AA.
 AC AU33200;
 XX 18-DEC-2001 (first entry)
 DE Novel human secreted protein #3691.
 KW Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 OS Homo sapiens.
 PN WO200179449-A2.
 PD 25-OCT-2001.
 PF 16-APR-2001; 2001MO-US08656.
 PR 18-APR-2000; 2000US-0552929.
 PR 26-JAN-2001; 2001US-0770160.
 PA (HYSE-) HYSEQ INC.
 PI Tang YT, Liu C, Dymnac RT;
 DR WPI: 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy -
 PS Claim 20; Page 729; 765pp; English.
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising
 CC the nucleic acids encoding the polypeptides and cells genetically
 CC engineered to express them are also useful for producing the proteins.
 CC The proteins are useful in genetic vaccination, testing and
 CC therapy, and can be used as nutritional supplements. They may be used to
 CC increase stem cell proliferation; to regulate haematopoiesis; and in
 CC bone, cartilage, tendon, and/or nerve tissue growth or regeneration;
 CC immune suppression and/or stimulation; as anti-inflammatory agents; and
 CC in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid
 CC sequences of novel human secreted proteins of the invention.
 XX Sequence 317 AA:
 Query Match 36.3%; Score 739; DB 22; Length 317;
 Best Local Similarity 54.8%; Pred. No. 1.2e-66;
 Matches 172; Conservative 17; Mismatches 93; Indels 32; Gaps 8;

OY 61 LHVQAGU-----ELPTSDPSVASOSARYRIGHHARLCLANPCGRNRYSLMCPMS 113
 DB 78 VSPCHSGLYNSRROMIPPSRPKVLDITGLAM-----PGLCLANPCGRNRYSLMCPMS 132
 OY 114 PELKOSTCLSLPKCWDYDRAAVPGFLFELHNRCPITLQDEYQWCHSLOPSTPEIKH 173
 DB 133 PELKOSTCLSLPKCWDYDRAAVPGFLFELHNRCPITLQDEYQWCHSLOPSTPEIKH 192
 OY 174 PPASASQVAGTKDMHHTWLI--FIFENELRQSLSVTOAGVWRNLSLOPLPPGFKL 231
 DB 193 PPASASQ--SSMDQRHAPLHLANFEYFEXFETESHVTRLESCGALIANCLPGSSY 250
 OY 232 FSCPSLSSMDYRRPRLANFEVFLVEMGF---TMFAR---LILISGCDLPPASASQ 283
 DB 251 SPAPASVXAGTTGAHRRILANFEVFLVEMGFHHVQVDARSIDLVIPLRP-----PKV 303
 OY 284 AGITGVSHHARLIF 297
 DB 304 LGLDVSHHRRAYF 317
 RESULT 12
 ID ABG21913 standard; Protein; 290 AA.
 AC ABG21913;
 XX 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #21904.
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PF 30-MAR-2001; 2001MO-US08631.
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Dymnac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 XX N-FSDB; AAS86100.
 CC New isolated polynucleotide and encoded polypeptides, useful in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits and to assess
 CC biodiversity -
 PS Claim 20; SEQ ID NO 52272; 103pp; English.
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.

Sequence 290 AA:

Query Match 36.1%; Score 735; DB 22; Length 290;
Best Local Similarity 47.6%; Pred. No. 2.7e-66;

Matches 182; Conservative 17; Mismatches 69; Indels 114; Gaps 12;

```
OY 6 LLPLECGAISAHNRLPGSSDSPASAPVAGITGCTHARLITFLVEMERLHVGQ 65
DB 11 LSPRLCEGSAISAHNRLCPSSDSPASR--ITGISGRHHAQLILVFLVEMRHHVQ 68
OY 66 AGLEPTSDPSVASASARVRYTHARLCLANFCGRNRVSLMCPSPMELKOSTCLSLP 125
DB 69 AGLKLTSGNP-----HH-----LGLP 85
OY 126 KCMQYRAAVGGLFLFLHRRCPLTODEVQWCDHSLQSTPEIKHPASASOVAGTK 185
DB 86 KCMQYSRKPP-----RPPRP-----101
OY 186 DMHHTWLIFFIFFLRQSLNSVTOAGVQWNLGSIQPLPPGFLFSCPSLSSMDYR- 244
DB 102 -----ITFFFLWMSLALVAQAGWQMDLSSLOPLPPGFEXFSCSLSRWMDYGC 152
OY 245 RPPRLANF-----VFLVEMGFTMEARL--ILISGPCDLPA-SASOSAGITGVSHHARL 295
DB 153 PPRRLANVCVQCVLVVDGFTMLARGLLELTSG--DLPPFGLPKCLGFTGMCHCARP 210
OY 296 IFNCLFEMESHSTQAGVQWPNIGSLOPLPPGLKRSCLSLPSSWDYGHLPHPANFC- 354
DB 211 IFFF--FEMESCFAVQAGVQWCDLSSLOPLPPRFKXFCSLSLSSMDYRHMPCLANCF 268
OY 355 -IFIRGVSPLYSGWSPDLR 375
DB 269 GFSRDRVSCGPRGSRTPDLK 290
```

RESULT 13
ABG68738 standard; Protein: 361 AA.

AC ABG68738;

DT 07-OCT-2002 (first entry)

DE Human prostate specific protein DEX0293_107.

Human; prostate specific nucleic acid; PSMA; prostate cancer; PSP;
prostate specific protein; cytosolic; non-cancerous prostate disease;
gene therapy; cancer; immunostimulant; vaccine.

OS Homo sapiens.

PN W020025735-A2.

PD 18-JUL-2002.

PF 27-NOV-2001; 2001WO-USA4363.

PR 27-NOV-2000; 2000US-253176P.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Machina RA, Recipon H, Cafferkey R, Ali S, Sun Y;

DR WPI; 2002-557831/59.

DR N-PSDB; ABK97631.

PT New prostate specific genes, useful for treating or diagnosing cancer,
or useful as vaccines for treating cancer, particularly prostate
cancer, in a patient

Claim 11; Page 207-208; 212pp; English.

The invention relates to a new isolated prostate-specific nucleic acid (PSNA) molecule comprising the cDNA sequences appearing as ABK97574-CC ABK97642 which encode prostate specific proteins appearing as CC ABK68701-ABG68746, or a sequence hybridizing to a PSNA or which has 60% sequence homology with a PSNA. Also included are a method of determining the presence of a PSNA in a sample, a vector comprising the PSNA, a host cell comprising the vector, producing the polypeptide encoded by the PSNA, a method of determining the presence of a PSP in a sample, diagnosing and monitoring the presence and metastases of prostate cancer in a patient, a kit for detecting a risk of cancer or presence of cancer in a patient (the kit comprising a means for determining the presence of the PSNA or PSP in a sample of a patient) and a vaccine comprising the polypeptide or the nucleic acid encoding the polypeptide. The PSNA, PSP and anti-PSP antibody are useful for diagnosing and treating cancer in a patient (e.g. by gene therapy). The nucleic acid molecule and polypeptide are also useful as vaccines for treating cancer, particularly prostate cancer and non-cancerous prostate diseases. The present sequence is a PSP of the invention.

Sequence 361 AA:

Query Match 36.1%; Score 734.5; DB 23; Length 361;
Best Local Similarity 43.1%; Pred. No. 4.1e-66;

Matches 185; Conservative 24; Mismatches 93; Indels 127; Gaps 12;

```
OY 6 LLPLECGAISAHNRLPGSSDSPASAPVAGITG-----CTHARL----- 49
DB 1 LLPRLECGITMAHORKLKLGSGLPASASRVGGTGMROPTMGTSCHAFQIGLPVAN 60
OY 50 -----ILVFLVEMERLHVGQAGLELTPSDPSVASASARVRYTHHARLCL 97
DB 61 FERSFYILGTSPLDMLINMF-----FALLIHVLF- 94
OY 98 NFCCGRNVSLMCP--SMSPELKOSTCLSLPKCMQYRAAVPGLFLFLHRRC----- 148
DB 95 -----NRDSCOPGASLTLGLEAFACLSLPCWMDYVRL-LPIDRFLQCCLSFPLN 148
OY 149 PTLTODEVQWCDHSLQSTPEIKHPASASOVAGTKDMHHTWLIFFIFNPLRQSLNS 208
DB 149 TVFQRAEV-----LIFQWMPVYLMSLSHS 172
OY 209 VTOAGVQWNLGSIQPLPPGFLFSCPSLSSMDYR-PPRLAN--FVFLVEMGFTMEA 265
DB 173 VAQAGVQWNCNIGSLOPLPPRRRRRFSCLSLSSMDHRAHAPCLANFLFKFLVDSFTMLA 232
OY 266 RLILISGPC-DLPASASOSAGITGVSH-----HARLIENFCLFEMES 306
DB 223 RLVLMSARSGLDLPAPASOSAGITGVHCTWPKSFADSHIGLAFHFAFFFFFAVAYS 292
OY 307 HSYVQAGVQWNLGSIQPLPPGLKRSCLSLPSSWDYGHLPHPANFCITFIRGVSPILS 366
DB 293 HPIAQAGVQWMDLGLAPPPEGKOFICLSLPGSDYRRAPRQANFCIFSDGVSFCWT 352
OY 367 GMSOTPDLR 375
DB 353 GMSOTPDLR 361
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RESULT 14
AAO10294 standard; Protein: 257 AA.

AC AAO10294;

DT 06-NOV-2001 (first entry)


```

Db      66 LKLPISGDLPASASOSAGI-TGVSHRAR----- 92
QY      126 KCM DYRAA AVGLF LFFL RHRCPT L TODEVOMCDHSS LQSTPEIKHP PASASQVAGTK 185
Db      93 -----PASSYLFFF-----XDEVSLC----- 108
QY      186 DMHHTW LFI FIFNF LROSLNSVTQAGVOMBNLGS LQPLPPGFKLFSCPSLSSMDYR 245
Db      109 -----CQAGVQLHDVGS LQ-LPPRFKRFSCPASRSSXDERR 143
QY      246 -PPRLANFVFLVENGFTMFARLILISGP-CDLPASASOSAGITGVSHHARLIENFCLFE 303
Db      144 LPPRLPNFCIFPMXRWGFITLARLVNSRPOCDLPASASOSAGITGVSHHARLPASSYCIFF 203
QY      304 MESH-SVTQAGVOMBNLGS LQPLPPGFKRFSCSLPSSMDYGHLPHPANFCIFIRGGVS 362
Db      204 LRMRLTIAQAGVXXCNCSS LQPPPTPGFKWVSCSLPSSMDYKSLPPLPANFCIFSRDGV 263
QY      363 PYLSGWSQTPDLR 375
Db      264 LCSLSMSRTPDPRK 276

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 Job time : 74 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2003, 07:50:41 ; Search time 338 Seconds
(without alignments)
8801.323 Million cell updates/sec

Title: US-09-380-203-1

Perfect score: 1442

Sequence: 1 TTTTGTGATGAGTGCAG.....TTAACAACGCTTAGACCA 1442

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published_Applications_MA:*

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- 15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1442	100.0	1442	11	US-09-964-666-1
2	1442	100.0	1442	11	US-09-964-412-1
3	1442	100.0	1442	12	US-09-964-667-1
4	1442	100.0	1442	12	US-09-872-968-1
5	1442	100.0	1442	15	US-10-146-130-1
6	1442	100.0	1442	15	US-10-092-934-1
7	1442	100.0	1442	15	US-10-153-334-53
8	1442	100.0	1442	15	US-10-198-069-48
9	1442	100.0	1442	15	US-10-198-070-125
10	1223.4	84.8	1418	11	US-09-964-666-4
11	1223.4	84.8	1418	11	US-09-964-412-4
12	1223.4	84.8	1418	12	US-09-964-667-4
13	1080.2	74.9	1381	11	US-09-964-666-3
14	1080.2	74.9	1381	11	US-09-964-412-3
15	1080.2	74.9	1381	12	US-09-964-667-3
16	587.8	40.8	65608	10	US-09-962-436-292

C 17	587.8	40.8	65608	11	US-09-962-832-119	Sequence 119, App
C 18	587.8	40.8	65608	11	US-09-954-531-180	Sequence 180, App
C 19	524.4	36.4	62944	11	US-09-954-456-2257	Sequence 2257, App
20	513	35.6	21470	11	US-09-764-847-1157	Sequence 1157, App
21	513	35.6	21470	15	US-10-092-154-1157	Sequence 1157, App
22	490.4	34.0	99014	11	US-09-880-107-3428	Sequence 3428, App
23	479.2	33.2	51719	10	US-09-918-686-2	Sequence 2, Appl1
24	479.2	33.2	92139	10	US-09-918-686-1	Sequence 1, Appl1
C 25	477.4	33.1	11319	12	US-09-764-872-579	Sequence 579, App
26	475.4	33.0	14796	11	US-09-954-456-973	Sequence 973, App
27	475.4	33.0	14796	11	US-09-954-456-1636	Sequence 1636, App
28	475.4	33.0	14796	11	US-09-918-186A-3	Sequence 3, Appl1
29	475.4	33.0	14796	11	US-09-880-107-3421	Sequence 3421, App
30	475.4	33.0	14796	15	US-10-138-618-35	Sequence 35, Appl1
31	475.4	33.0	26657	10	US-09-810-673A-3	Sequence 3, Appl1
C 32	471.2	32.7	12542	11	US-09-764-864-1774	Sequence 1774, App
C 33	467	32.4	15041	10	US-09-764-869-1421	Sequence 1421, App
C 34	467	32.4	15041	15	US-10-091-504-1421	Sequence 1421, App
C 35	464.8	32.2	57130	11	US-09-835-081-3	Sequence 3, Appl1
C 36	447.8	31.1	14176	11	US-09-764-864-1644	Sequence 1644, App
37	440.8	30.6	13224	10	US-09-764-853-897	Sequence 897, App
38	440.6	30.6	23106	12	US-09-863-049A-1	Sequence 1, Appl1
39	440.2	30.5	110096	11	US-09-880-107-1542	Sequence 1542, App
C 40	439.2	30.5	110096	11	US-09-880-107-1542	Sequence 1542, App
41	436.4	30.3	118067	14	US-10-081-327-32	Sequence 32, Appl1
42	436.2	30.2	2226	15	US-10-027-632-102037	Sequence 102037, App
C 43	433.2	30.0	20247	11	US-09-764-877-2680	Sequence 2680, App
C 44	433	30.0	32148	12	US-09-764-881-6806	Sequence 6806, App
C 45	429.8	29.8	27148	10	US-09-764-860-1046	Sequence 1046, App

ALIGNMENTS

RESULT 1
US-09-964-666-1
Sequence 1, Application US/09964666
Patent No. US20020104108A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Wands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for Screening Drugs Effective for the Treatment or Prevention of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,666
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

Mon Jul 21 09:56:17 2003

us-09-380-203-1.rnpb

Page 2

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? TOPOLOGY: bcch
? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 15..1139
? SEQUENCE DESCRIPTION: SEQ ID NO: 1
US-09-964-666-1

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Query Match:	100.0%;	Score 1442;	DB 11;	Length 1442;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1442;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

OY	1	TTTTTTTTTTTTTTGAGATGAGAGTTTGGCTTGTGTTGGCCAGGCGATGAGATGGAATGGCCGAA	60
Dp	1	TTTTTTTTTTTTTTGAGATGAGAGTTTGGCTTGTGTTGGCCAGGCGATGAGATGGAATGGCCGAA	60
OY	61	TCCTACGCACCCGCAACCTCCGCTCCCGGGGTTTAAACGATTCCTCGTCACACCTCCG	120
Dp	61	TCCTACGCACCCGCAACCTCCGCTCCCGGGGTTTAAACGATTCCTCGTCACACCTCCG	120
OY	121	CAGTAGCGGGATTTAACAGCATGTGACCCACCGCTGGGTAATTTGATTTTTTTTAA	180
Dp	121	CAGTAGCGGGATTTAACAGCATGTGACCCACCGCTGGGTAATTTGATTTTTTTTAA	180
OY	181	TAGAGATGTGAGTTTCTCATGTGTTGGTCAGAGCTGTGCTCGAAGTCCCGACTTCAGATATC	240
Dp	181	TAGAGATGTGAGTTTCTCATGTGTTGGTCAGAGCTGTGCTCGAAGTCCCGACTTCAGATATC	240
OY	241	CCCTCCGTCGCGCTCCCAAAGTGTAGATACAGAGCTGGCCACCATGCGCCGGCTCGCC	300
Dp	241	CCCTCCGTCGCGCTCCCAAAGTGTAGATACAGAGCTGGCCACCATGCGCCGGCTCGCC	300
OY	301	TGGCTAATTTTTTGTGTAGAAACAGAGGTTTACGAATGTGCCCCAGAGCTGTCTCTAGC	360
Dp	301	TGGCTAATTTTTTGTGTAGAAACAGAGGTTTACGAATGTGCCCCAGAGCTGTCTCTAGC	360
OY	361	TCGAACAGTCCACTGTGCTACAGCTCCCAAAGTCTGTGGATTACAGAGGCTCACCCGCTGC	420
Dp	361	TCGAACAGTCCACTGTGCTACAGCTCCCAAAGTCTGTGGATTACAGAGGCTCACCCGCTGC	420
OY	421	CTGGGCTTTTATTTTATTTTTTTTAAACACAGAGGTGTCCACTGTTCACCGAGATGAG	480
Dp	421	CTGGGCTTTTATTTTATTTTTTTTAAACACAGAGGTGTCCACTGTTCACCGAGATGAG	480
OY	481	TCGACTGTGTGATCACAGCTCAGTCAGACGCTTAACCTCTGAGATCAAGAGCTCTCTG	540
Dp	481	TCGACTGTGTGATCACAGCTCAGTCAGACGCTTAACCTCTGAGATCAAGAGCTCTCTG	540
OY	541	CCTCAGGCTCCCAAGTAGCTGGGAGCCAAAGACATGACACCATCTACCTGTGCTAATTTTTTA	600
Dp	541	CCTCAGGCTCCCAAGTAGCTGGGAGCCAAAGACATGACACCATCTACCTGTGCTAATTTTTTA	600
OY	601	TTTTTATTTTAAATTTTTTATGACAGAGTCTCAACTGTCTACCCAGGCTGAGTGCAGT	660
Dp	601	TTTTTATTTTAAATTTTTTATGACAGAGTCTCAACTGTCTACCCAGGCTGAGTGCAGT	660
OY	661	GGCGCAATCTTGGCTACATGCAACCTCCGCTCCCGGGTTCAAGTTATTTCTCGGCCCA	720
Dp	661	GGCGCAATCTTGGCTACATGCAACCTCCGCTCCCGGGTTCAAGTTATTTCTCGGCCCA	720
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Dp	721	GGCTCTAGTAGCTGGAGCTACAGAGCCGACACAGCCCTAGTGTAAATTTTTTGTATTTT	780
OY	781	TAGTAGAGATGAGGTTTACCATGTTCGCGACAGTTGATCTTGAATCTGTGACCTTGTATC	840
Dp	781	TAGTAGAGATGAGGTTTACCATGTTCGCGACAGTTGATCTTGAATCTGTGACCTTGTATC	840
OY	841	TGCGCTGCTCGGCTCCCAAGTCTGGGATTTACAGGCGTGAAGCCACACAGCCGCGCTTA	900
Dp	841	TGCGCTGCTCGGCTCCCAAGTCTGGGATTTACAGGCGTGAAGCCACACAGCCGCGCTTA	900
OY	901	TTTTTAATTTTGTGTGTTGAATGTCACTGTGTTACCCAGGCTGAGTGCAT	960

Db	901	TTTTTAATTTTTTGTGTTGTAATAATGAAATTCACCTGATTACCGAGAGCTGGAGTGCATAT	960
Oy	961	GGCCCAATATTCGGCTCAGTGCACACCTCGCTCCCGGGCTCAAGAGATTCCTGTCTCA	1020
Db	961	GGCCCAATTCGGCTCAGTGCACACCTCGCTCCCGGGCTCAAGAGATTCCTGTCTCA	1020
Oy	1021	GGCTCCCAAGACAGTGGGATTACGGGGACCGTGCACACACCCCGCATTTTGTATTT	1080
Db	1021	GGCTCCCAAGACAGTGGGATTACGGGGACCGTGCACACACCCCGCATTTTGTATTT	1080
Oy	1081	TCATTAGAGCGGGGTTTACCATATTTGTGACGTGGTCCAAACCTCGACCTAGGT	1140
Db	1081	TCATTAGAGCGGGGTTTACCATATTTGTGACGTGGTCCAAACCTCGACCTAGGT	1140
Oy	1141	GAACCCACCTGCCTCAGCCTCCCAAGTGTGGATTACAGGGCTGAGCCACCTCACCCAG	1200
Db	1141	GAACCCACCTGCCTCAGCCTCCCAAGTGTGGATTACAGGGCTGAGCCACCTCACCCAG	1200
Oy	1201	CCGGCTAATTTAATATAAAAAATATGATAGCAATGGGGGGTCTTGCTATGTTGGCCAGCT	1260
Db	1201	CCGGCTAATTTAATATAAAAAATATGATAGCAATGGGGGGTCTTGCTATGTTGGCCAGCT	1260
Oy	1261	GGTTCCAAACTCTGGACTCATGCAATCCTTCCAAATGAGGCACACACCAGCCAGCTA	1320
Db	1261	GGTTCCAAACTCTGGACTCATGCAATCCTTCCAAATGAGGCACACACCAGCCAGCTA	1320
Oy	1321	CATTTTAAACAGTACATCTTATATTTAGTATACTAAGAGATATACAAATAAACATGT	1380
Db	1321	CATTTTAAACAGTACATCTTATATTTAGTATACTAAGAGATATACAAATAAACATGT	1380
Oy	1381	CAAACTGCAAAATCTAGTAGTACAGAGTCTTTTATACCTTTTAAACAAAGCTTAGAG	1440
Db	1381	CAAACTGCAAAATCTAGTAGTACAGAGTCTTTTATACCTTTTAAACAAAGCTTAGAG	1440
Oy	1441	CA 1442	
Db	1441	CA 1442	

RESULT 2
 US-09-964-412-1
 : Sequence 1. Application US/09964412
 : Patent No. US20020129391A1
 :
 GENERAL INFORMATION:
 APPLICANT: de la Monte, Suzanne
 Wands, Jack R.
 TITLE OF INVENTION: Transgenic Animals and Cell Lines for
 Screening Drugs Effective for the Treatment or Prevention
 of Alzheimer's Disease
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P. L. L. C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/964,412
 FILING DATE: 28-Sep-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Remond, Robert W.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0609,4370000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600

ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert W.
 REGISTRATION NUMBER: 52, 893
 REFERENCE/DOCKET NUMBER: 0609, 4370000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1442 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 15..1139
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-964-667-1

Query Match 100.0%; Score 1442; DB 12; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1442: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGTGATGAGGATTTGCTGTTGTTGCCAGGCTGAGTGCATGCGCGCA 60
 DB 1 TTTTGTGATGAGGATTTGCTGTTGTTGCCAGGCTGAGTGCATGCGCGCA 60
 QY 61 TCTAGCTCACCCGACCTCCGCTCCGGGTTCAAGCATGCTCTGCTGAGCTGCC 120
 DB 61 TCTAGCTCACCCGACCTCCGCTCCGGGTTCAAGCATGCTCTGCTGAGCTGCC 120
 QY 121 CAGTAGCTGGATTAGAGCATGTCACCCAGCTGGGCAATTTGTAATTTTATG 180
 DB 121 CAGTAGCTGGATTAGAGCATGTCACCCAGCTGGGCAATTTGTAATTTTATG 180
 QY 181 TAGAGTGAATTTCTCATGTTGCTGAGCTGCTGCTGAGTCCGACCTGATG 240
 DB 181 TAGAGTGAATTTCTCATGTTGCTGAGCTGCTGCTGAGTCCGACCTGATG 240
 QY 241 CCTCCGCTCGGGCTCCCAAGTGTCTAGATGACAGTGGCCACATGCGGCTG 300
 DB 241 CCTCCGCTCGGGCTCCCAAGTGTCTAGATGACAGTGGCCACATGCGGCTG 300
 QY 301 TGGCTAATTTTGTGTAGAACAGAGGTTTCACTGATGTGCCAAGCTGTCT 360
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 QY 361 TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTCAGAGCTGAG 420
 DB 361 TCAAGCAGTCCACCTGCTCAGCTCCCAAGTGTGGGATTCAGAGCTGAG 420
 QY 421 CTGGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
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 QY 481 TGCAGTGTGTGATGACAGTCTACGACGCTTCACTGATGATGCTGATG 540
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 DB 661 GGGCAATCTTGGCTACTGCAACCTGCTCCGGGTTCAAGTATTTCTCTCC 720
 QY 721 GCTTCTGATGAGTGGGACTACAGGCGCCACACGCTAGTATTTTATTTT 780

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 DB 781 TACTAGAGTGGGCTTACCATGTTGCGCAGGTTGATCTGATGACCTTGTGATC 840
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 DB 841 TGGCTGCTCGGCTCCCAAGTAGTGGGATTAAGAGGCTGAGCAGCAGCCGCTTA 900
 QY 901 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 960
 DB 901 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 960
 QY 961 GGGCAATCTGAGCTGCAACCTGCTCCGGGTTCAAGTATTTCTCTCC 1020
 DB 961 GGGCAATCTGAGCTGCAACCTGCTCCGGGTTCAAGTATTTCTCTCC 1020
 QY 1021 GCTTCCCAAGCAGTGGGATTAAGAGGCTGAGCAGCAGCAGCTAATTTT 1080
 DB 1021 GCTTCCCAAGCAGTGGGATTAAGAGGCTGAGCAGCAGCAGCTAATTTT 1080
 QY 1081 TCATTAGAGGCGGCTTCAACATTTTGTGAGGCTGCTGCTCAAACTCTGAC 1140
 DB 1081 TCATTAGAGGCGGCTTCAACATTTTGTGAGGCTGCTGCTCAAACTCTGAC 1140
 QY 1141 GACCCACCTGCTGAGCTTCAACAGTGGGATTAAGAGGCTGAGCAGCAG 1200
 DB 1141 GACCCACCTGCTGAGCTTCAACAGTGGGATTAAGAGGCTGAGCAGCAG 1200
 QY 1201 CGGGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTTAGTAAATTT 1260
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 QY 1261 GGTCTCAAACTTGTGCTTCAAGCATCTTCCCAAGTGGGACCAAGCCAG 1320
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 DB 1321 CATTTTAAACAGTAACTTTATTTATTTATTTATTTATTTATTTATTT 1380
 QY 1381 CAACCTGCAAACTGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1440
 DB 1381 CAACCTGCAAACTGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1440
 QY 1441 CA 1442
 DB 1441 CA 1442

RESULT 4
 US-09-872-968-1
 ; Sequence 1, Application US/09872968
 ; Publication No. US20030050262A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wands, Jack R
 ; TITLE OF INVENTION: Inhibition of Neurodegeneration
 ; FILE REFERENCE: 21486-047
 ; CURRENT APPLICATION NUMBER: US/09/872,968
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 1442
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-872-968-1

Query Match 100.0%; Score 1442; DB 12; Length 1442;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 1442: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 361 TCAAGCAGTCCAGCTGCTGAGCTCCCAAGTGTGGATTAACAGGCTGACGCTGTC 420
Db 361 TCAAGCAGTCCAGCTGCTGAGCTCCCAAGTGTGGATTAACAGGCTGACGCTGTC 420
Oy 421 CTGGCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCACTCTTTACCCAGATGAG 480
Db 421 CTGGCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCACTCTTTACCCAGATGAG 480
Oy 481 TGCAGTGTGTGATCAGAGCTCAGCTGAGCCTTCACTCTGAGATCAAGATCTCTG 540
Db 481 TGCAGTGTGTGATCAGAGCTCAGCTGAGCCTTCACTCTGAGATCAAGATCTCTG 540
Oy 541 CCTAGCCTCCCAAGTACCTGGAGCAACAAAGATCAACATCACTGAGCTGATTTTGA 600
Db 541 CCTAGCCTCCCAAGTACCTGGAGCAACAAAGATCAACATCACTGAGCTGATTTTGA 600
Oy 601 TTTTATTTTATTTTATTTTGAAGACAGAGTCAACTGTGACCCAGGCTGAGTGCAGT 660
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Oy 661 GGGCCAAATCTGGCTCACTGCAACCTGCTCCCGGTTCAAGTATTTCTGCCCCA 720
Db 661 GGGCCAAATCTGGCTCACTGCAACCTGCTCCCGGTTCAAGTATTTCTGCCCCA 720
Oy 721 GCTCTCTAGTAGCTGGGACTACAGGCGCCACCAAGCTAGTAAATTTTGTATTTT 780
Db 721 GCTCTCTAGTAGCTGGGACTACAGGCGCCACCAAGCTAGTAAATTTTGTATTTT 780
Oy 781 TAGTAGAGATGGGTTACCATGTTCCGACAGTTGATCTTGTGACCTGTGTATC 840
Db 781 TAGTAGAGATGGGTTACCATGTTCCGACAGTTGATCTTGTGACCTGTGTATC 840
Oy 841 TGGCTGCTCGGCTCCCAAGTGTGGGATTAAGGGGTGAGCCACACCCCGGCTTA 900
Db 841 TGGCTGCTCGGCTCCCAAGTGTGGGATTAAGGGGTGAGCCACACCCCGGCTTA 900
Oy 901 TTTTAAATTTTGTGTTGTAAGATGAAATCTCACTGTTACCCAGGCTGGAGTGCAT 960
Db 901 TTTTAAATTTTGTGTTGTAAGATGAAATCTCACTGTTACCCAGGCTGGAGTGCAT 960
Oy 961 GGGCAATCTGCGCTCACTGCAACCTGCTCCCGGCTCAAGGATTCCTGCTCTCA 1020
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Db 1021 GCTGCCAAGAGCTGGGATTAAGGGGCACTGCCACACACCCGCTAATTTTGTATT 1080

Oy 1081 TCATTAGAGGGGGTTTACCATTATTTGTCAGGCTGCTCAAACTCCTGACCTCAGGT 1140
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Oy 1261 GGTCTCAAACTTCTGCTTCAATGCAATCTTCCAAATGAGCAGACACCCAGCAGTCA 1320
Db 1261 GGTCTCAAACTTCTGCTTCAATGCAATCTTCCAAATGAGCAGACACCCAGCAGTCA 1320
Oy 1321 CATTTTAAACAGTTTACATCTTTATTTTATATATAGTAAAGTAAATTAACATGT 1380
Db 1321 CATTTTAAACAGTTTACATCTTTATTTTATATATAGTAAAGTAAATTAACATGT 1380
Oy 1381 CAACCTGCAATTCAGTAGTAACAGAGTCTTTTATATACCTTTTAAACAGCTTTAG 1440
Db 1381 CAACCTGCAATTCAGTAGTAACAGAGTCTTTTATATACCTTTTAAACAGCTTTAG 1440
Oy 1441 CA 1442
Db 1441 CA 1442

RESULT 5
US-10-146-130-1
; Sequence 1, Application US/10146130
; Publication No. US20030004107A1
; GENERAL INFORMATION:
; APPLICANT: AVERBACK, PAUL
; TITLE OF INVENTION: METHOD OF PREVENTING CELL DEATH USING SEGMENTS OF
; FILE OF INVENTION: NEURAL THREAD PROTEINS
; FILE REFERENCE: 59003.000007
; CURRENT APPLICATION NUMBER: US/10/146,130
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1:
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15)..(1139)
US-10-146-130-1

Query Match 100.0%; Score 1442; DB 15; Length 1442;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1442: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TTTTGTGAGATGAGTTTGGCTCTGTTGCCAGGCTGGATGCAATGGCGAA 60
Db 1 TTTTGTGAGATGAGTTTGGCTCTGTTGCCAGGCTGGATGCAATGGCGAA 60
Oy 61 TCTCAGCTACACGGAACCTCCGCTCCGGGTTCAAGGATTCCTGCTCAGGCTCC 120
Db 61 TCTCAGCTACACGGAACCTCCGCTCCGGGTTCAAGGATTCCTGCTCAGGCTCC 120
Oy 121 CAGTAGCTGGGATTAACAGGATGTCACCCAGCTCCGCTAATTTGATTTTGTAG 180
Db 121 CAGTAGCTGGGATTAACAGGATGTCACCCAGCTCCGCTAATTTGATTTTGTAG 180
Oy 181 TAGAGATGAGTTTCTCATGTTGGTGGCTGGCTGGAAGTCCGACCTCAGATGATC 240
Db 181 TAGAGATGAGTTTCTCATGTTGGTGGCTGGCTGGAAGTCCGACCTCAGATGATC 240
Oy 241 CCTCGCTCGGCTCCCAAGTGTAGATACAGAGCTGGCCAGCATTGCCGCTCTGCC 300

[illegible]

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Db 901 TTTTAAATTTTGTGTTTGAATGAATCTCACTGTGTACCAAGCTGAGTGCAT 960
Qy 961 GGGCAATCTGCGCTCACTGCAACCTGCTGCCGGGCTCAAGGATTCCTCTCA 1020
Db 961 GGGCAATCTGCGCTCACTGCAACCTGCTGCCGGGCTCAAGGATTCCTCTCA 1020
Qy 1021 GCTCCCAAGCAGCTGGGATTCAGGAGCCTGCCACACACCCGCTAATTTTGTATT 1080
Db 1021 GCTCCCAAGCAGCTGGGATTCAGGAGCCTGCCACACACCCGCTAATTTTGTATT 1080
Qy 1081 TCATTAGAGCGGGGTTTACCAATATTTGTAGGCTGCTCAAACTCTGACCTCAGGT 1140
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Db 1201 CCGGCTAATTTAGATTAATAAATAATATAGCAATGGGGGCTTGTATTTGCCAGGCT 1260
Qy 1261 GGTCTCAAACTTGGGCTTCAATGCAATCTTCCAAAGTCCCAACACACCCAGCAGTCA 1320
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Qy 1381 CAACCTGCAAAATTCAGTAGTACAGAGTCTTTTATTAATTTTAAACAGCTTTAGAG 1440
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Qy 1441 CA 1442
Db 1441 CA 1442

RESULT 9

US-10-198-070-125
: Sequence 125, Application US/10198070
: Publication No. US20030109437A1
: GENERAL INFORMATION:
: APPLICANT: AVERBACK, PAUL
: APPLICANT: GEMMELL, JACK
: TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER
: TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF
: FILE REFERENCE: 59003.000008
: CURRENT APPLICATION NUMBER: US/10/198,070
: PRIOR APPLICATION NUMBER: 60/306,161
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/306,150
: PRIOR FILING DATE: 2001-07-19
: PRIOR APPLICATION NUMBER: 60/331,477
: PRIOR FILING DATE: 2001-11-16
: NUMBER OF SEQ ID NOS: 125
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 125
: LENGTH: 1442
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (15) .. (1139)
US-10-198-070-125

Query Match 100.0%: Score 1442: DB 15: Length 1442:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 1442: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 TTTTATTTTGTGATGAGTTTTCGCTGTGTTGCCAGGCTGGAGTGCATAGGCGCA 60
Db 1 TTTTATTTTGTGATGAGTTTTCGCTGTGTTGCCAGGCTGGAGTGCATAGGCGCA 60
Qy 61 TCTAGCTCACCGCAACCTCCGCTCCGGGTTCAAGGATTCCTCTCAGCCTCC 120
Db 61 TCTAGCTCACCGCAACCTCCGCTCCGGGTTCAAGGATTCCTCTCAGCCTCC 120
Qy 121 CAGTAGCTGGATTAACAGCATGTGCACCCAGCTGCGCTAATTTTGTATT 180
Db 121 CAGTAGCTGGATTAACAGCATGTGCACCCAGCTGCGCTAATTTTGTATT 180
Qy 181 TAGAGATGAGTTTCTCATGTGTTGCTAGGCTGGCTCGCAACTCCGACCTAGATATC 240
Db 181 TAGAGATGAGTTTCTCATGTGTTGCTAGGCTGGCTCGCAACTCCGACCTAGATATC 240
Qy 241 CCTCGCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCATGCGGCTCTGCC 300
Db 241 CCTCGCTCGGCTCCCAAGTGTAGATACAGACTGGCCACCATGCGGCTCTGCC 300
Qy 301 TGGCTAATTTTGTGATGAAACAGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC 360
Db 301 TGGCTAATTTTGTGATGAAACAGGTTTCACTGATGTGCCAAGCTGGTCTCTGAGC 360
Qy 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTAACAGGCTGAGCGCTGC 420
Db 361 TCAAGCAGTCCACCTGCTCAGCCTCCCAAGTGTGGGATTAACAGGCTGAGCGCTGC 420
Qy 421 CTGGCTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
Db 421 CTGGCTTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 480
Qy 481 TGCAGTGTGTATACAGCTTCACTGACGCTTCAACTCTGATGATCAAGCATCTCTCTG 540
Db 481 TGCAGTGTGTATACAGCTTCACTGACGCTTCAACTCTGATGATCAAGCATCTCTCTG 540
Qy 541 CCTCAGCTCCCAAGTACGTGGAGCAACCAAGATGCACTACACCTGAGCTAATTTT 600
Db 541 CCTCAGCTCCCAAGTACGTGGAGCAACCAAGATGCACTACACCTGAGCTAATTTT 600
Qy 601 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
Db 601 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 660
Qy 661 GGGCAATCTGCGCTCACTGCAACCTGCTGCCGGGTTCAAGTATTCCTGCCCCA 720
Db 661 GGGCAATCTGCGCTCACTGCAACCTGCTGCCGGGTTCAAGTATTCCTGCCCCA 720
Qy 721 GCTTCCTAGTAGCTGGAGTACAGGCGCCACACGCTAGCTAATTTTGTATT 780
Db 721 GCTTCCTAGTAGCTGGAGTACAGGCGCCACACGCTAGCTAATTTTGTATT 780
Qy 781 TAGTAGAGATGGGCTTACACATGTTCCGCAAGTTGATCTGATCTGACCTGTGATC 840
Db 781 TAGTAGAGATGGGCTTACACATGTTCCGCAAGTTGATCTGATCTGACCTGTGATC 840
Qy 841 TGCCTGCTGGGCTCCCAAGTGTGGATTACAGGGGTAGGCCACACCCGCGCTTA 900
Db 841 TGCCTGCTGGGCTCCCAAGTGTGGATTACAGGGGTAGGCCACACCCGCGCTTA 900
Qy 901 TTTTATTTTGTGTTTGAATGAAATGCAATCTGTTACCAGGCTGGAGTGCAT 960
Db 901 TTTTATTTTGTGTTTGAATGAAATGCAATCTGTTACCAGGCTGGAGTGCAT 960
Qy 961 GGGCAATCTGCGCTCACTGCAACCTGCTCCGGGCTCAAGGATTCCTCTCA 1020
Db 961 GGGCAATCTGCGCTCACTGCAACCTGCTCCGGGCTCAAGGATTCCTCTCA 1020
Qy 1021 GCTTCCTCAAGCAGCTGGGATTCAGGAGCCTGCCACACACCCGCTAATTTTGTATT 1080
Db 1021 GCTTCCTCAAGCAGCTGGGATTCAGGAGCCTGCCACACACCCGCTAATTTTGTATT 1080

QY 1081 TCATTAGAGCGGGGTTTCACCATTTGTCAGGCTGCTCTCAAACTCTGACCTCAGGT 1140
 DB 1081 TCATTAGAGCGGGGTTTCACCATTTGTCAGGCTGCTCTCAAACTCTGACCTCAGGT 1140
 QY 1141 GACCCACCTGCTGCTGCTTCCAAAGTCTGGAATTCAGGCGTGCACACCTCAGGT 1200
 DB 1141 GACCCACCTGCTGCTGCTTCCAAAGTCTGGAATTCAGGCGTGCACACCTCAGGT 1200
 QY 1201 CCGGCTAATTTAGATTAATTAATGATGCAATGGGGGCTTGTGATGTTGCCAGGCT 1260
 DB 1201 CCGGCTAATTTAGATTAATTAATGATGCAATGGGGGCTTGTGATGTTGCCAGGCT 1260
 QY 1261 GGTCTCAAACTTCTGCTTCATGCAATCTTCCAAATGAGCCACACACCCAGGCTCA 1320
 DB 1261 GGTCTCAAACTTCTGCTTCATGCAATCTTCCAAATGAGCCACACACCCAGGCTCA 1320
 QY 1321 CATTTTAAACAGTTTCACTCTTATTTAGTATCTAGAAATTAATTAATTAATTAAT 1380
 DB 1321 CATTTTAAACAGTTTCACTCTTATTTAGTATCTAGAAATTAATTAATTAATTAAT 1380
 QY 1381 CAACCTGCAATTTCACTAGTAAACAGTCTTTTAACTTTTAAACAAAGCTTAGG 1440
 DB 1381 CAACCTGCAATTTCACTAGTAAACAGTCTTTTAACTTTTAAACAAAGCTTAGG 1440
 QY 1441 CA 1442
 DB 1441 CA 1442

RESULT 10

US-09-964-666-4
 Sequence 4, Application US/09964666
 Patent No. US20020104108A1
 GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
 Hands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for
 Screening Drugs Effective for the Treatment or Prevention
 of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: DC

COUNTRY: USA
 ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/964,666
 FILING DATE: 28-Sep-2001
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Esmond, Robert M.
 REGISTRATION NUMBER: 32,893
 REFERENCE/DOCKET NUMBER: 0609,4370000

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2540
 TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1418 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both

MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-964-666-4

Query Match 84.8%; Score 1223.4; DB 11; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

QY 2 TTTTATTTTGGAGATGAGTTTGGCTTTGCTTTGTCACAGCTGAGTGAATGGCGAAT 61
 DB 1 TTTTATTTTGGAGATGAGTTTGGCTTTGCTTTGTCACAGCTGAGTGAATGGCGAAT 60
 QY 62 CTCACCTACCGCAACCTCCGCTCCGGGTTCAAGGATTTCTCCCTCACCCTCCC 121
 DB 61 CTCACCTACCGCAACCTCCGCTCCGGGTTCAAGGATTTCTCCCTCACCCTCCC 120
 QY 122 AGTA-GCTGGATTAAGAGGATGTCACCCACAGCTGCTAATTTGTAATTTTGTAG 180
 DB 121 AGTAGGCTGGATTAAGAGGATGTCACCCACAGCTGCTAATTTGTAATTTTGTAG 179
 QY 181 TAGAGATGAGTTTCTCCATGTTGTCAGCTGCTGCGAATCTCCGACCTCAGATGATC 240
 DB 180 TAGAGATGAGTTTCTCCATGTTGTCAGCTGCTGCGAATCTCCGACCTCAGATGATC 238
 QY 241 CCTCGCTGCGGCTCCCAAGTCTGATGATACAGACTGCGCCACATGCGCGG-CTCTGC 299
 DB 239 CTCCGCTGCGGCTCCCAAGTCTGATGATACAGACTGCGCCACATGCGCGGCTCTGC 298
 QY 300 CTGCTAATTTTGTGATGAAGACAGGTTTCACTGATGTCGCAAGCTGCTCTGAG 359
 DB 299 CTGCTAATTTTGTGATGAAGACAGGTTTCACTGATGTCGCAAGCTGCTCTGAG 358
 QY 360 CTCACAGCTGCAACCTGCGCTCCAGCTCCCAAGTCTGCGGATTAAGGCTGACGCGGTG 419
 DB 359 CTCACAGCTGCAACCTGCGCTCCAGCTCCCAAGTCTGCGGATTAAGGCTGACGCGGTG 418
 QY 420 CTTGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 479
 DB 419 CTTGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 478
 QY 480 GTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 539
 DB 479 GTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 537
 QY 540 GCGTACAGCTGCC-AAGTAGCTGGGACCAAGACATGACATGACATGACATGATTTT 598
 DB 538 GCGTACAGCTGCCAAGTAGCTGGGACCAAGACATGACATGACATGACATGATTTT 597
 QY 599 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 658
 DB 598 TATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 657
 QY 659 GTGGGCAATCTTGGCTCAGTCAACCTGCTCCGCGGTTCAAGTATTTCTCTGCC 718
 DB 658 GTGGGCAATCTTGGCTCAGTCAACCTGCTCCGCGGTTCAAGTATTTCTCTGCC 717
 QY 719 CAGGCTCGTGGATGAGCGGACCTACAGGCGCCACAGCGCTAATTTTATTTTATTTT 778
 DB 718 CAGGCTCGTGGATGAGCGGACCTACAGGCGCCACAGCGCTAATTTTATTTTATTTT 777
 QY 779 TTAGAGAGATGGGG-TTCACCATGTTGCGAGTTGAT-CTGATCTCTGACCTGT 836
 DB 778 TTAGAGAGATGGGGTTTCACCATGTTGCGAGTTGATCTGATCTCTGACCTGT 837
 QY 837 GATGCTCGCTGCGCTGCTCCCAAGTCTGAGATTAAGG-CGTGAGCAGCAGCGCGG 895
 DB 838 GATGCTCGCTGCGCTGCTCCCAAGTCTGAGATTAAGGCGTGAAGCGCGCGG 897
 QY 896 GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 955
 DB 898 GCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 957
 QY 956 GCAATGGCCAAATCTGCTCAGTCAACCTGCTCCGCGGCTCAAGGATTTCTCTG 1015
 DB 958 GCAATGGCCAAATCTGCTCAGTCAACCTGCTCCGCGGCTCAAGGATTTCTCTG 1017
 QY 1016 TCTCAGCTCCCAAGAGCTGGGATTAAGGCGACCTGCGCACACACCCGCTAATTTT 1075

Db	1018	TCTGACGCTCCCAAGCAGCTGGGATACGGGCACCTG-CACACACCCCGCTAATTTTGG	1076
QY	1076	TATTTTCATTAGAGCGGGGTTTTACCATATTTGTCAAGGCTGGTCTCAAACTCCTGACCT	1135
Db	1077	TATTTTCATTAGAGCGGGGTTTTACCATATTTGTCAAGGCTGGTCTCAAACTCCTGACCT	1136
QY	1136	CAGGTGACCCACAGCTGCCTCAGCCCTTCCAAAGTGTGGGATTACAGGCGTGAGCCACCTCA	1195
Db	1137	CAGGTGACCCACAGCTGCCTCAGCCCTTCCAAAGTGTGGGATTACAGGCGTGGA--GGCCTCA	1194
QY	1196	CCCAAGCCGGGCTAATTTAGATATAAAAATATGTAGCAATGGGGGGCTTTGCTATGTTGGCC	1255
Db	1195	CCCAAGCCGGGCTAATTTAGATATAAAAATATGTAGCAATGGGGGGCTTTGCTATGTTGGCC	1254
QY	1256	AGGCTGGTCTCAAACTTCTGGCTTCATGCAATCTCTTCCAAATGAGCCACAACCCAGCC	1315
Db	1255	AGGCTGGTCTCAAACTTCTGGCTTCATGCAATCTCTTCCAAATGAGCCACAACCCAGCC	1314
QY	1316	AGTCACATTTTTTAAACAGTTACATCTTTATTTTAGTACTAGAAATATACAAATAA	1375
Db	1315	AGTCACA-TTTTTTAAACAGTTACATCTTTATTTTAGTACTAGAAATGATACGATAAC	1373
QY	1376	CATGCAACCTGCAGAAATTCAGTAGTACAGAGTCTCTT	1414
Db	1374	ATGGCGGAAGCTGCAGAAATTCAGTAGTACAGAGTCTCTT	1412

Db 1018 TCTACGCTCCCAAGCAGCTGGGATTAAGGGACCTG-CACACACCCCGTAATTTTGG 1076
QY 1076 TATTTTCATTAAGAGGGGGTTTTCACATATTTGTCAGCTGCTCAAACTCTGACCT 1135
Db 1077 TATTTTCATTAAGAGGGGGTTTTCACATATTTGTCAGCTGCTCAAACTCTGACCT 1136
QY 1136 CAGTGTACCCAGCTGCTGACCTTCGCAAGTGTGGATTAAGAGGAGAGGACCACTCA 1195
Db 1137 CAGTGTACCCAGCTGCTGACCTTCGCAAGTGTGGATTAAGAGGAGAGGACCACTCA 1194
QY 1196 CCCAGCCGGCTAATTAAGTAAATAATATGACATGGGGGCTCTGCTATGTTGCC 1255
Db 1195 CCCAGCCGGCTAATTAAGTAAATAATATGACATGGGGGCTCTGCTATGTTGCC 1254
QY 1256 AGGCTGTCTCAAACTCTGCTTCATGCAATCTTCCTCAATGAGCCACACACCCAGCC 1315
Db 1255 AGGCTGTCTCAAACTCTGCTTCATGCAATCTTCCTCAATGAGCCACACACCCAGCC 1314
QY 1316 AGTCACATTTTAAACAGTATCATCTTATTTAGTATCTAGAAAGTAAATACATTA 1375
Db 1315 AGTCACA-TTTTAAACAGTATCATCTTATTTAGTATCTAGAAAGTAAATACATTA 1373
QY 1376 CATGTCAAACTGCAATTCAGTATGACAGATCTTT 1414
Db 1374 ATGGCGAGACCTGCAATTCAGTATGACAGATCTTTT 1412

RESULT 12
US-09-964-667-4
Sequence 4, Application US/0964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Mands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609.4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-964-667-4

Query Match 84.8%; Score 1223.4; Db 12; Length 1418;
Best Local Similarity 96.9%; Pred. No. 0;

Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;
QY 2 TTTTATTTTGAATGAGATTTTTCGCTCTGTTGCCAGAGCTGAGTGCATAGCCCAT 61
Db 1 TTTTATTTTGAATGAGATTTTTCGCTCTGTTGCCAGAGCTGAGTGCATAGCCCAT 60
QY 62 CTCAGCTCACCGACACCTCGCTCCCGGGTTTCAAGGATTTCTGCTCCACCTCCCC 121
Db 61 CTCAGCTCACCGACACCTCGCTCCCGGGTTTCAAGGATTTCTGCTCCACCTCCCC 120
QY 122 AGTA-GCTGGATTTACAGCATGTGCACCCAGCTGCGCTAATTTTATTTTGA 180
Db 121 AGTAAAGCTGGATTTACAGCATGTGCACCCAGCTGCGCTAATTTTATTTTGA 179
QY 181 TAGAGATGAGATTTCTCATGTTGTGACGGCTGTCTGCAACTGCCACCTCAGATATC 240
Db 180 TAGAGATGAGATTTCTCATGTTGTGACGGCTGTCTGCAACT-CGACCTCAGATATC 238
QY 241 CTCGCTGCTGGCTCCCAAGTGTAGATACAGAGTGGCAGCATGCCCGG-CTCTGC 299
Db 239 CTCGCTGCTGGCTCCCAAGTGTAGATACAGAGTGGCAGCATGCCCGGCTCTGC 298
QY 300 CTGGCTAATTTTGTGTGTAAGAAAGGTTTCACTGATGTGCCAAGCTGTCTCTGAG 359
Db 299 CTGGCTAATTTTGTGTGTAAGAAAGGTTTCACTGATGTGCCAAGCTGTCTCTGAG 358
QY 360 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGATTACAGGCGTGCAGCCGTG 419
Db 359 CTCAGCAGTCCACCTGCTCAGCTCCCAAGTGTCTGGATTACAGGCGTGCAGCCGTG 418
QY 420 CTTGGCTTTTATTTTATTTTATTTTAAAGACAGGTGTCCCATCTTACCGAGATGA 479
Db 419 CTTGGCTTTTATTTTATTTTATTTTAAAGACAGGTGTCCCATCTTACCGAGATGA 478
QY 480 GTGACAGTGTGTATGACAGCTACCTGACGCTTAACTCTGAGATCAAGCATCTCTCT 539
Db 479 GTGACAGTGTGTATGACAGCTACCTGACGCTTAACT-CTGAGATCAAGCATCTCTCT 537
QY 540 GCTCTAGCTGCC-AACTAGCTGGAGCAACACATGACACCTACCTAGCTAATTTT 598
Db 538 GCTCTAGCTGCCAAAGTACTGGAGCAACACATGACACCTACCTAGCTAATTTT 597
QY 599 TATTTTATTTTATTTTATTTTGAAGAGTCTCAACTCTGTACCCAGGCTGAGATGA 658
Db 598 TATTTTATTTTATTTTATTTTGAAGAGTCTCAACTCTGTACCCAGGCTGAGATGA 657
QY 659 GTGGGCAATCTTGCTCACTGCAACTGTGCTCTCCGGGTTCAAGTATTTCTCTGCC 718
Db 658 GTGGGCAATCTTGCTCACTGCAACTGTGCTCTCCGGGTTCAAGTATTTCTCTGCC 717
QY 719 CAGCTCTGAGTAACTGAGACTACAGGCGCCACACAGCTTACCTAATTTTGTAT 778
Db 718 CAGCTCTGAGTAACTGAGACTACAGGCGCCACACAGCTTACCTAATTTTGTAT 777
QY 779 TTTAGTAAAGTGGG-TTCACCATGTTGGCAGGTTGAT-CTGATGCTGACCTT 836
Db 778 TTTAGTAAAGTGGGTTTACCATGTTGGCAGGTTGATCTGATGCTGACCTT 837
QY 837 CATCTGCTGCTGCTGCTCCCAAGTGTGAGATTAAGG-CGTGAGCCACACCCCGG 895
Db 836 CATCTGCTGCTGCTGCTCCCAAGTGTGAGATTAAGGAGTGTGAGCCACCCCGG 897
QY 896 GCTTATTTTATTTTGTGTTTGAATGGAATCTACCTGTACCCAGGCTGAGT 955
Db 895 GCTTATTTTATTTTGTGTTTGAATGGAATCTACCTGTACCCAGGCTGAGT 957
QY 956 GCAATGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1015
Db 955 GCAATGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1017
QY 1016 TCTACGCTCCCAAGCAGCTGGGATTAAGGGACCTG-CACACACCCCGTAATTTTGG 1075
Db 1015 TCTACGCTCCCAAGCAGCTGGGATTAAGGGACCTG-CACACACCCCGTAATTTTGG 1076

OY 1076 TATTTTCATTAGAGCGGGGTTTCACATATTTGTGACGCTGCTCAAACTCCTGACCT 1135
 DB 1077 TATTTTCATTAGAGCGGGGTTTCACATATTTGTGACGCTGCTCAAACTCCTGACCT 1136
 OY 1136 CAGGTGACCACTGCTGACGCTTCCAAAGTGTGGGATTACAGGCGTACCTCA 1195
 DB 1137 CAGGTGACCACTGCTGACGCTTCCAAAGTGTGGGATTACAGGCGTACCTCA 1194
 OY 1196 CCGACCGGCTAATTTAATAAATAATGTAGCAATGGGGGCTTGTCTATGTTGCC 1255
 DB 1195 CCGACCGGCTAATTTAATAAATAATGTAGCAATGGGGGCTTGTCTATGTTGCC 1254
 OY 1256 AGGCTGCTCAAACTTGTGCTCATGCAATCTTCCAAATGAGCCCAACACCCAGCC 1315
 DB 1255 AGGCTGCTCAAACTTGTGCTCATGCAATCTTCCAAATGAGCCCAACACCCAGCC 1314
 OY 1316 AGTCACATTTTAAACAGTTACATCTTTTATTTAGTACTAGAAAGTAAATCAATAA 1375
 DB 1315 AGTCACA-TTTTAAACAGTTACATCTTTTATTTAGTACTAGAAAGTAAATCAATAA 1373
 OY 1376 CATGCAACCTGCAATTTCACTAGTACTAGAGGCTCTT 1414
 DB 1374 ATGGCGAACCCTGCAATTTCACTAGTACTAGAGGCTCTT 1412

RESULT 13

US-09-964-666-3

Sequence 3, Application US/09964666

Patent No. US20020104108A1

GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne

Mands, Jack R.

TITLE OF INVENTION: Transgenic Animals and Cell Lines for

Screening Drugs Effective for the Treatment or Prevention

of Alzheimer's Disease

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/964,666

FILING DATE: 28-Sep-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Esmund, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 0609.4370000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1381 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-964-666-3

Query Match 74.9%; Score 1080.2; DB 11; Length 1381;
 Best Local Similarity 94.4%; Fred. No. 2.6e-304;
 Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;

OY 2 TTTTGTGATGAGAGTTTTCCTCTGTTGGCCAGGCTGAGTGAATGGGCAAT 61
 DB 1 TTTTGTGATGAGAGTTTTCCTCTGTTGGCCAGGCTGAGTGAATGGGCAAT 60
 OY 62 CTCACCTACCGCAACCTCCGCTCCGCGTTCAAGCAATTCCTGCTCAGCTCCCC 121
 DB 61 CTCACCTACCGCAACCTCCGCTCCGCGTTCAAGCAATTCCTGCTCAGCTCCCC 120
 OY 122 AGTACCTGGGATTACAGGATGTGCACCCAGCCTGGGCTAATTTGTTATTTT 181
 DB 121 AGTACCTGGGATTACAGGATGTGCACCCAGCCTGGGCTAATTTGTTATTTT 179
 OY 182 AGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTGCAACCTCCGCTCAGATGT 239
 DB 180 AGAGATGGAGTTTCTCCATGTTGGTCAAGCTGGTCTGCAACCTCCGCTCAGATGT 239
 OY 240 CCGTCCGCTCGGCTCCCAAGTGTCT--AGATACAGGACTGGCCACATGCCGG--CT 295
 DB 240 CCGTCCGCTCGGCTCCCAAGTGTCTGATTTACAGGATGAGCCACATGCCGGCT 299
 OY 296 CTGCTGCTGCTAATTTTGTGTTAGAAACAGGTTTCACTGATG-TGCCAAGCTGCTC 354
 DB 300 CTGCTGCTGCTAATTTTGTGTTAGAAACAGGTTTCACTGATGTTGCCAAGCTGCTC 359
 OY 355 CTGACCTCAAGCAGTCACTGCTCAGCTCCCAAGGCTGGGATTACAGGCTGTCAG 414
 DB 360 CTGACCTCAAGCAGTCACTGCTCAGCTCCCAAGGCTGGGATTACAGGCTGTCAG 418
 OY 415 CCGTCCGCTGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 474
 DB 419 CCGTCCGCTGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 478
 OY 475 ATGAGTCAAGTGTGATATCACTGCTCAGCTCCCAAGGCTGGGATTACAGGCTGTCAG 533
 DB 479 ATGAGTCAAGTGTGATATCACTGCTCAGCTCCCAAGGCTGGGATTACAGGCTGTCAG 538
 OY 534 CCGTCCGCTGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 593
 DB 539 CCGTCCGCTGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 597
 OY 594 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 653
 DB 598 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 656
 OY 654 GTGCAAGTGGGCAATCTTGGCTCACTGCAACCTTGGCTCCGCGTTCAAGTATTTTCC 713
 DB 657 GTGCAAGTGGGCAATCTTGGCTCACTGCAACCTTGGCTCCGCGTTCAAGTATTTTCC 716
 OY 714 TGCCTCAGCTCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 773
 DB 717 TGCCTCAGCTCCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 776
 OY 774 GTATTTTATTTAGATGAGTGGG-TTCACCATGTTGCCAGGTTGATCTGATCTGACAC 832
 DB 777 GTATTTTATTTAGATGAGTGGGTTTCACCATGTTGCCAGGTTGATCTGATCTGACAC 836
 OY 833 TTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
 DB 837 TTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
 OY 892 CCGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 951
 DB 895 CCGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 954
 OY 952 GAGTCAATGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
 DB 955 GAGTCAATGG-CAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
 OY 1012 CCTGCTCAGCTCCCAAGCAGCTGGGATTACGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071
 DB 1013 CCTGCTCAGCTCCCAAGCAGCTGGGATTACGGG-ACGTGACACACACCCCGCTAATT 1070

QY	2 TTTTATTTTGAACATGATGATTTTGCGCTTGTGGTCCACAGCTGGAGTGCANATGGCCAT	61
Dp	1 TTTTATTTTGAATGAGATTTTGCGCTTGTGGTCCACAGCTGGAGTGCANATGGCCAT	60
QY	62 CTCAGCTACCGCAACATCCGCGTCCGGGTTCAGACGATTCCTGCTCAACCTCCGC	121
Dp	61 CTCAGCTACCGCAACCTCCGCTCCGGGTTCAGACGATTCCTGCTCAACCTCCGC	120
QY	122 AGTACGTGGATTTACAGGCATGTGACCCAGCCTCGGCTAATTTGTATTTTTTTTAACT	181
Dp	121 AGTACGTGGATTTACAGGCATGTGCA -CCAGCGCTGGCTAATTTGTATTTTTTTTAACT	179
QY	182 AGAGATGAGATTT -CTCATGTTGGTACAGCTGGTCTGCAACTCCGACCTCGATGAT	239
Dp	180 AGAGATGAGATTTAACTCATGTTGGTACAGCTGGTCTGCAACTCCGACCTCGATGAT	239
QY	240 CCGTCCGCTGCGGCGCTCCCAAGTGCCT - -AGATTACAGCATGGCCACATGGCCGG -CT	295
Dp	240 CCGCGCTGCGGCTCCCAAGTGTGATTTACAGGCATGACCATGCGCGGCT	299
QY	296 CTGCGCTGGCTAATTTTGTGGTATGAAACAGGTTTACTGATG -TGCCCAAGCTGGTCTC	354
Dp	300 CTGCGCTGGCTAATTTTGTGGTATGAAACAGGTTTACTGATGTTGCCAAGCTGGTCTC	359
QY	355 CTGAGCTCAAGCAGTCCACGCTGCTCAGCCTCCCAAGTGTGGATTTACAGGCGTGCAG	414
Dp	360 CTGAGCTCAAGCAGCTCAGCTGCTCAGCCTCCCAAGTGTGGATTTACAGGCGT -CAG	418
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Dp	419 CCGAGCTCGGCGCTTTTATTTTATTTTATTTTAAAGACAGGCTGTCACATCTTACCCAG	478
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Dp	479 ATGAAGTGCAGTGTGTGATCCAGACCTAGCAGCTTCAACCTCGAATATCAACAT	538
QY	534 CCTCCTGCTCAACCTCCCAAGTAGCTGGGACCAAGAATATGCACACTACCTGAGCTA	593
Dp	539 CCTCCTGCTCAACCTCCCAAGTAGCTGGGACCAAGAATATGCACACTACCTGAGCTG -TA	597
QY	594 ATTTTATTTTATTTTATTTTATTTTGAAGACAGAGTCTCAACTGTGCACCCAGGCTGGA	653
Dp	598 ATTTTATTTTATTTTATTTTATTTTGAAGACAGAGTCT -ACTGTGCACCCAGGCTGGA	656
QY	654 GTGCAGTGGGCGCATCTTGACTCAACCTCTCCCTCCCGGGTTCAAGTTATTTCTCC	713
Dp	657 GTGCAGTGGGCGCATTTGGCTCACTCAACCTCTCCCTCCCGGGTTCAAGTTATTTCTCC	716
QY	714 TGCCCCAGGCTCTGATGATGCTGGAGCTAAAGCGGCCACACAGCGCTAGTATTTTTT	773
Dp	717 TGCCCCAGGCTCTGATGATGCTGGAGCTAAAGCGGCCACACAGCGCTAGTATTTTTT	776
QY	774 GTATTTTAAATAGATGGGG -TTCCACATGTTCGCAAGTTGATCTTGATCTGTGAC	832
Dp	777 GTATTTTAAATAGATGGGGTTTCCACATGTTCGCAAGTTGATCTTGATCTGTGAC	836
QY	892 CCGCGCTTATTTTATTTTGTGTTTGAATGGAATCACTGCTATACACAGGCTG	951
Dp	895 GCGCGCTTATTTTATTTTGTGTTTGAATGGAATCACTGCTATACACAGGCTG	954
QY	833 TTGTGATCTGCTGCTCGGCT -CCCAAGTGTGGGATTAACAGGCGTAGCCACACG	891
Dp	837 TTGTGATCTGCTGCTCGGCTACCCCAAGTGTGGGATTAACG -GTGTGACTGCAC	894
QY	952 GAGTGCAGTATTTTATTTTGTGTTTGAATGGAATCACTGCTATACACAGGCTG	1011
Dp	955 GAGTGCAGTATG -CAATATCGGCTATCTGCGCAACTGTGCTCCGGG -TTAAGCATTTCT	1012
QY	1012 CCTGTCTCAACCTCCCAAGCAGCTGGGATTAAGGCGACCTGCGACACACACCCGCTAAT	1071
Dp	1013 CCTGTCTCAACCTCCCAAGCAGCTGGGATTAAGGCG -ACTGTCAACACACCCGCTAAT	1070
QY	1072 TTTGTATTTTCAATTAGAGCGGAGTTCACACATTTGTGCAAGCT -GCTCTCAACTCT	1130

Db 1071 TTTGATTTTCATGAGCGGG--TTTACATATTTCAGGCTGGGCTCAACTCT 1128
Qy 1131 GACCTCAGGTGACCCACTGCTGCTTCCAAAGTCTGGATTACAGCGGTGACCA 1190
Db 1129 GACCTCAGGTGACCCACTGCTGCTTCCAAAGTCTGGATTACAGCGGTGACCA 1188
Qy 1191 CCTCAGCGGCTGATTTAGATAAATAATGATGCAATGGGGGTCTGTATGT 1250
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Db 1247 TGCCAGGCTGCTTCAACTCTGCTTCAATGCAATCTTCCAAATGAGCCACACAC 1306
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Qy 1371 ATAAACATGTCAAC 1385
Db 1367 ATAAACATGTCAAC 1381

RESULT 15
US-09-964-667-3
Sequence 3, Application US/09964667
Publication No. US20030033621A1
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
Mands, Jack R.
TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/964,667
FILING DATE: 28-Sep-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0609,4370000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1381 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-964-667-3

Query Match 74.9% Score 1080.2; DB 12; Length 1381;
Best Local Similarity 94.4%; Pred. No. 2,6e-304;
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;
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Qy 1012 CCGTCTGAGCTTCCCAAGCAGCTGAGATTACAGGACCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
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Mon Jul 21 09:56:17 2003

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Page 16

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Db	1247	TGGCCAGGCTGTGTCAAACTGTGGCTGTATGCAATCCTTCGAAATGAGCCCAACAC	1306
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Oy	1371	ATAAATCATGTCAAC	1385
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Search completed: July 20, 2003, 09:20:31
Job time : 341 secs

Job time : 341 secs

TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 14..1418
 PCT-US95-17111A-120

Query Match 84.8% Score 1223.4; DB 5; Length 1418;
 Best Local Similarity 96.9%; Pred. No. 0;
 Matches 1375; Conservative 0; Mismatches 31; Indels 13; Gaps 12;

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 1376 CATGCAACCTGCAAAATTCAGTACTACAGGCTCTT 1414
 1374 ATGGCGGAACCTGCAAAATTCAGTACTACAGGCTCTT 1412

RESULT 5
 US-08-454-557C-49
 Sequence 49 Application US/0845457C
 Patent No. 5830670
 GENERAL INFORMATION:
 APPLICANT: de la Monte, Suzanne
 APPLICANT: Wands, Jack R.
 TITLE OF INVENTION: Neutral Thread Protein Gene Expression and Detection
 TITLE OF INVENTION: of Alzheimer's Disease
 NUMBER OF SEQUENCES: 121
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 STREET: 1100 New York Avenue, Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/454,557C
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0609,3840003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1381 base pairs
 TYPE: nucleic acid

Query Match 74.9%; Score 1080.2; DB 2; Length 1381;
 Best Local Similarity 94.4%; Pred. No. 3.5e-292;
 Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;

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Db 1 TTTTATTTTATGAGATGAGTTTGGCTCTTGTGGCCAGGCTGAGTCGAATGGCGCAAT
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OY 62 CTCAGCTACCGCAACCTCCGCGTCCGGGTTCAAGGATTTCTCTGCTCAGCTCCGCC
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Db 61 CTCAGCTACCGCAACCTCCGCGTCCGGGTTCAAGGATTTCTCTGCTCAGCTCCGCC
   |||||||
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Db 837 TTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
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Db 895 GCGGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
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OY 952 GAGTGCATTTGCGCAATCTGCGCTACATGCAACCTGCTCCCGGGTCAAGGATTTCT
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Db 1013 CCTGTCTCAGCTCCCAAGCATGAGTGTACGGG--ACGTGCACACACCCCGCTAAT
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RESULT 7
 US-08-450-673C-49
 : Sequence 49, Application US/08450673C
 : Patent No. 5948888
 : GENERAL INFORMATION:
 : APPLICANT: de la Monte, Suzanne
 : APPLICANT: Wands, Jack R.
 : TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
 : NUMBER OF SEQUENCES: 121
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
 : STREET: 1100 New York Avenue, Suite 600
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: U.S.A.
 : ZIP: 20005-3934
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/450,673C
 : FILING DATE: 30-MAY-1995
 : CLASSIFICATION: 530
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ludwig, Steven R.
 : REGISTRATION NUMBER: 36,203
 : REFERENCE/DOCKET NUMBER: 0609,3840004
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 371-2600
 : TELEFAX: (202) 371-2540
 : INFORMATION FOR SEQ ID NO: 49:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1381 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: both
 : TOPOLOGY: both
 : US-08-450-673C-49

Query Match 74.9%; Score 1080.2; DB 2; Length 1381;
 Best Local Similarity 94.4%; Pred. No. 3.5e-292;
 Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;


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OY 2 TTTTGTGATGAGATGTTTGGCTCTGTGTCAGGCTGAGTGCATGAGCGCAT 61
DB 1 TTTTGTGATGAGATGAGATGTTTGGCTCTGTGTCAGGCTGAGTGCATGAGCGCAT 60
OY 62 CTCAGCTACCGCAACCTCCGCTCCGCGGTCAAGCAATTCCTGCTCAGCTCCGCC 121
DB 61 CTCAGCTACCGCAACCTCCGCTCCGCGGTCAAGCAATTCCTGCTCAGCTCCGCC 120
OY 122 AGTAGCTGAGATGATGAGGATGTCACCGCAGCTGCGCTAATTTGTTATTTT 181
DB 121 AGTAGCTGAGATGATGAGGATGTCACCGCAGCTGCGCTAATTTGTTATTTT 179
OY 182 AGAGATGAGATGTTTCTCATGTGTGTCAGGCTGCTGCACTCCAGCTCAGATGAT 239
DB 180 AGAGATGAGATGTTTCTCATGTGTGTCAGGCTGCTGCACTCCAGCTCAGATGAT 239
OY 240 CCGTCCGCTGCGCTCCCAAGTCTCT--AGATACAGAGCTGCGCAGCTCCGCGG--CT 295
DB 240 CCGTCCGCTGCGCTCCCAAGTCTCTAGATGATGAGGATGAGGCTCAGCTCCGCGGCT 299
OY 296 CTGCTGCTGCTAATTTTGTGTAGAAAGAGGTTTCACTGATG--TGCCCAAGCTGCTC 354
DB 300 CTGCTGCTGCTAATTTTGTGTAGAAAGAGGTTTCACTGATGTTGCCAAGCTGCTC 359
OY 355 CTGAGCTAAGCAGTCCACCTGCTCAGCTCCCAAGTCTGCGGATTAAGGCGCTGAG 414
DB 360 CTGAGCTAAGCAGTCCACCTGCTCAGCTCCCAAGTCTGCGGATTAAGGCGGT--CAG 418
OY 415 CCGTCCGCTGCGCTTTTATTTATTTTAAAGCAAGTGTCCCTTTTACCCAGG 474
DB 419 CCGTCCGCTGCGCTTTTATTTATTTTAAAGCAAGTGTGACCACTTTACCCAGG 478
OY 475 ATGAAGTCAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 533
DB 479 ATGAAGTCAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 538
OY 534 CCGTCCGCTGCGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 593
DB 539 CCGTCCGCTGCGCTCCCAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 597
OY 594 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 653
DB 598 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 656
OY 654 GTGAGTGTGCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 713
DB 657 GTGAGTGTGCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
OY 714 TGCCCAAGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 773
DB 717 TGCCCAAGCTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 776
OY 774 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 832
DB 777 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 836
OY 833 TTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
DB 837 TTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
OY 892 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 951
DB 895 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
OY 952 GAGTGTGATGCGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011
DB 955 GAGTGTGATGCG--CAAAATCTGCGCTACTGCAACCTGCTCCCGGG--TCAAGGATCT 1012
OY 1012 CCGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1071
DB 1013 CCGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1070
OY 1072 TTTGATTTTATTTATTTAGAGCGGCTTTTCAACATATTTTGTGAGCT--GCTGTCAACGCT 1130

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DB 1071 TTTGATTTTATTTATTTAGAGCGGG--TTTACATATTTTGTGAGGCTGCTGCTCAAACTCCT 1128
OY 1131 GAGCTCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
DB 1129 GAGCTCAGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1188
OY 1191 CCTCAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1250
DB 1189 CCTCAGCTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1246
OY 1251 TGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1310
DB 1247 TGCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1306
OY 1311 CAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
DB 1307 CAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1366
OY 1371 ATTAACATGTCAAC 1385
DB 1367 ATTAACATGTCAAC 1381

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RESULT 8
PCT-US95-17111A-49
; Sequence 49, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/17111A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/340,426
; FILING DATE: 14-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
PCT-US95-17111A-49

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OY Query Match 74.9%; Score 1080.2; DB 5; Length 1381;
Best Local Similarity 94.4%; Pred. No. 3,5e-292;
Matches 1317; Conservative 0; Mismatches 53; Indels 25; Gaps 18;
2 TTTTGTGATGAGATGTTTGGCTCTGTGTCAGGCTGAGTGCATGAGCGCAT 61
TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

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Db 1 TTTTGTGAGAGAGAGTTTGGCTGTGTTGCCAGGCTGAGATGCAATGGCGCAAT 60
OY 62 CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGGATTTCTGCGCTCACCTCCCC 121
Db 61 CTCAGCTCACCGCAACCTCCGCTCCCGGGTTCAAGGATTTCTGCGCTCACCTCCCC 120
OY 122 ACTAGCTGGGATTTACAGGATGTGACCCAGCTCGGCTAATTTTATTTTATTTTAT 181
Db 121 ACTAGCTGGGATTTACAGGATGTGACCCAGCTCGGCTAATTTTATTTTATTTTAT 179
OY 182 AAGAGATGAGTTT - CTCATGTGTGTGACAGCTGTGTGTGAGTCTCCGAGCTAGAT 239
Db 180 AAGAGATGAGTTTACATGTGTGTGTGAGTCTGTGAGTCTCCGAGCTCTGATGAT 239
OY 240 CCTCGCTGCGGCTCCCAAGTGT - AGATACAGAGTGTGCGCCAGTGGCGG - CT 295
Db 240 CTCGCTGCTGCGGCTCCCAAGTGTGAGATTTACAGGATGTGAGTGTGCGGCT 299
OY 296 CTGCTGCTGCTAATTTTGTGTGAGAAACAGGGTTTCTGATG - TGCCCAAGCTGTGCTC 354
Db 300 CTGCTGCTGCTAATTTTGTGTGAGAAACAGGGTTTCTGATGTGTGCGCAAGCTGTGCTC 359
OY 355 CTGAGCTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 414
Db 360 CTGAGCTCAAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 418
OY 415 CCGTGGCTGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 474
Db 419 CCGTGGCTGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 478
OY 475 ATGAGTGTGAGT 533
Db 479 ATGAGTGTGAGT 538
OY 534 CCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 593
Db 539 CCGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
OY 594 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 653
Db 598 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 656
OY 654 GTGAGTGTGCGCAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 713
Db 657 GTGAGTGTGCGCAATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
OY 714 TGCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 773
Db 717 TGCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
OY 774 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 832
Db 777 GTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 836
OY 833 TTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 891
Db 837 TTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
OY 892 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
Db 895 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954
OY 952 GAGTGCATGAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Db 955 GAGTGCATGAG - CAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1012
OY 1012 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1071
Db 1013 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070
OY 1072 TTTGTATTTTCAATTGAGGCGGGGTTTCCACATATTGTGACGCT - GGTCTCAAACTCCT 1130
Db 1071 TTTGTATTTTCAATTGAGGCGGG - TTTACCAATTTTGTGAGGCTGTGCTCAAACTCCT 1128

OY 1131 GACCTCAGGTGAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1190
Db 1129 GACCTCAGGTGAGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1188
OY 1191 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1250
Db 1189 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1246
OY 1251 TGCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1310
Db 1247 TGCCCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1306
OY 1311 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1370
Db 1307 CCGTGTCTGAGCTCCCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1366
OY 1371 ATTAACATGTCAAC 1385
Db 1367 ATTAACATGTCAAC 1381

RESULT 9

US-08-975-080-35
; Sequence 35, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; NUMBER OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7176
; TELEFAX: 202-467-7000
; INFORMATION FOR SEQ. ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14796 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-975-080-35

Query Match 33.0%; Score 475.4; DB 4; Length 14796;
Best Local Similarity 69.8%; Pred. No. 7.8e-123;
Matches 877; Conservative 0; Mismatches 321; Indels 59; Gaps 15;

OY 1 TTTTGTGAGAGAGTTTGGCTGTGTTGCCAGGCTGAGATGCAATGGCGCA 60
Db 5380 TTTTGTGAGAGAG - TTTGACCTGTGTTGCCAGGCTGAGATGCAATGGCGCA 5438

QY	6	TCCTCAGCTCAGCGAACCCTCGCGCTCCCGGGTTCAAGCATTTCTCTGCTCAGCCTCC	120
Db	5439	TCCTGGCTACAGCAACCTCTCTCTCGGGTTCAAGTATTTCTCTGCTCAGCCTCC	5498
QY	121	CAGTACGTGGGATTTACAGGCATGTGCACCCAGCGCTCGGCTAATTTTGGTATTTTTCG	180
Db	5499	AAGTAACTGGGATTTACAGGGAAGTGCACACACCAGCTAATTTT---TGATTTTTCG	5555
QY	181	TAGACATGAGCTTCTCCATGTTTGGTCAGGCTGTGCTCGAATCTCCGACCTCAGATGATC	240
Db	5556	TAGACATGGGGTTTACACCATTTGGCCAGGCTGGTGTGAATCTCTGACCTC---GTGATT	5613
QY	241	CTCCGCTCGGCGCTCCCAAAATGCTAGATTAACAGACATGCGGCACCATGCGCGCTGCG	300
Db	5614	CGCCACCCCTGGCGCTCCCAAAATGCTG---GATTACAGCGCTGAACACACACCGCCTGCG	5678
QY	301	TGGCTAATTTTGTGTGGTAAACACAGGTTTCACTATGTGCCCAAGCTGTCTCCTG---	357
Db	5671	TTTTTTTTTTTGTGTTCT---GAGACACAGTTTTCATCTGTATCCACGCTGGAGTACGGTGG	5722
QY	358	--AGCTCAGACGATCCACCTGCGCTCAGCCTCCCAAGAGTCTGGATTTACAGCGTGGACG	415
Db	5730	CCTGATTTCTCGAATTCATCGAATCCTCGCCTCTCTGGGCTCAGTGAATTTGCTGCTTCAAC	5785
QY	416	CTGCGCTGCGCTTTTATTTATTTATTTTAAAGACACAGGTGTCCCATCTTACCCAGGA	475
Db	5790	CTCCCAATAGCGCGAATTTACAGGCATGTGCGCACACACCGCATTAATTTTGTATTTT	5845
QY	476	TGAATGTGAGTGGTGTGATCA---CAGTCTACGACGCTTCATCTCTGAGATCAAG---CA	532
Db	5850	GGTAGAGACGAGGTTTACACATGTTTGGCAGGCTGTTTGAATCTCTGACCTCAGGGA	5905
QY	533	TCCTCTGCTCTCAGGCTCCCAAGTAGTGGGACCAAAAGACATGACACCACTACACTGGC-	591
Db	5910	TCCACCCGCTCAGGCTCCCAAAAGTGTGAGATTTATAGTGTGAGCCACACACCTGGCC	5965
QY	592	-----TAATTTTATTTTATTTTATTTTATTTTGTGACAGAGTCTCACTCTGT	640
Db	5970	TCAGGAATATTTTATTTATTTTAAATTTATTTATTTTATTTTGAAGTGAATGTC---TGCTGCT	6028
QY	641	CACCCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACTGGAACCTCTGCTCCCGGGTT	700
Db	6029	CGCCAGGCTTAGAGTGCAGCAGCGGAGTCTCGGCTCACTGGAAGCTCCGCCCGCAGGT	6088
QY	701	CAGTATTTCTCTGAGCCCGCCAGCTCCCTGAGTAGTGGGAGATACAGAGCG---CACACAG	757
Db	6089	CAGCGCATTTCTCTGCTCAGGCTCCGAGTAGTGGGAGATACAGGCGCCCGCACACA	6148
QY	758	CTAGACTAATTTTGTATTTTATTTAGTAGAGATGGG---GTACACATGTTCCACAGGTGA	816
Db	6149	CCCGGCTAATTTTGTATTTTATTTAGTAGAGACGGGTTTACCGGTGTACAGAGAGG	6208
QY	817	TCCTGATCTCGAGACTGTGATCTGCTGCTCGGCTCCCAAGTCTGGGATTTACG	876
Db	6209	TCCTGATCTCTGAGCTCTGATCTGCTGCTCGGCTCCCAAGTCTGGGATTTACG	6268
QY	877	GCGTAGGACACAGCGCGCTAATTTTAAATTTTGTGTTGTTGAATGGAATGATCACT	936
Db	6269	GTTGAGGACACACACCGCGCT-----ATTTTATTTTGTGAGACAGGACTACT	6320
QY	937	CTGTTACCAAGGCTGGAGTGCATATGCGCAATCTGGCTCACTCAACCTCTGCTCCG	996
Db	6321	CTGTACCTGGGCTGAGTGCAGTGG---TACACATAGCTCACTGAGGCTCGAATCTCTG	6379
QY	997	GGCTCAGAGCATTTCTCTGCTCAGGCTCCCAAGCAGCTGGGATTTAGGGCACTGCCAC	1056
Db	6380	AGCTCAGAGCATTTCTCTCAGCTCTCAATCTCTCAACAGTATTTGGAGCTACAGGTGACCCAC	6439
QY	1057	CACACCCCGCTAATTTTGTAT-----TTATATAGAGGGCGGGTTCAC	1101
Db	6440	CATGCCACCAATTTATTTATTTATTTATTTATTTATTTATTTATTCATAGAGATGAGGCTTCC	6499
QY	1102	CATATTTGTACGGCTGCTCAAACTCTGACCTCAGGTGACCCACCGCTCGCCTCAGCCTTC	1161

Db	Seq	Score	DB	Length
Db	6500 TGTGTTGTCCAGGCTGCTGTTTGAACCTCTGACCTCAGGAGATCCTTTTGGCTGGGCTCC	6555		
QY	1162 CAAATGCTGGGATTAACAGGCGGTGAGCCACCTCACCACCGCGCTAATTTAGATATAA	1218		
Db	6560 CAAATGCTGAGATTACAGGCAATGAGCCACCGTCCAGCTTAGAATCATTTTAA	6616		
<p>RESULT 10</p> <p>US-09-630-706-10</p> <p>; Sequence 10, Application US/09630706</p> <p>; Patent No. 6277640</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: C. Frank Bennett</p> <p>APPLICANT: Lex M. Cowsett</p> <p>TITLE OF INVENTION: ANTISENSE MODULATION OF HER-3 EXPRESSION</p> <p>FILE REFERENCE: RTS-0053</p> <p>CURRENT APPLICATION NUMBER: US/09/630,706</p> <p>CURRENT FILING DATE: 2000-08-01</p> <p>NUMBER OF SEQ ID NOS: 94</p> <p>SEQ ID NO 10</p> <p>LENGTH: 14796</p> <p>TYPE: DNA</p> <p>ORGANISM: Homo sapiens</p> <p>FEATURE:</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (2811)...(2921)</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (3174)...(3283)</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (5158)...(5275)</p> <p>NAME/KEY: CDS</p> <p>LOCATION: (11955)...(12044)</p> <p>US-09-630-706-10</p>				
<p>Query Match 33.0%; Score 475.4; DB: 4; Length 14796;</p> <p>Best Local Similarity 69.8%; Pred. No. 7.8e-123;</p> <p>Matches 877; Conservative 0; Mismatches 321; Indels 59; Gaps 15;</p>				
QY	1 TTTTGTGAGATGAGATTTTGGCTCTTTGTTGCCCCAGGCTGAGTGCATGGCCAA	60		
Db	5380 TTTTGTGAGATGAGATTTTGGCTCTTTGTTGCCCCAGGCTGAGTGCATGGCCAA	5438		
QY	61 TCTAGCTCAGCCGCAACCTCCGCTCCGCGGTCAAGGATTTCCGCTCAGCCCTCC	120		
Db	5439 TCTTGGCTCAGTGAACCTCTGCTCTGCGGTTAAAGATTTCTGCTCAGCCCTCC	5498		
QY	121 CAGTAGCTGGGATTACAGGATGTGACCCACGCTCGGCTAATTTTGTATTTTAA	180		
Db	5499 AAGTAAGTGGGATTACAGGAGGACCCACACCCAGCTAATTTT--TGATTTTAA	5555		
QY	181 TAGAGATGAGATTTCTCATGTGTGTCAGGCTGTCGAACCTCCGACCTCAGATATC	240		
Db	5556 TAGAGATGAGGATTTACACCACTTTGCCAGGCTGCTGTAAGTCTTACCTC--GTGATT	5613		
QY	241 CCTCCGCTGCGCTCCCAAAAGTCTAGATACAGAGACTGGCCACATGCCCCGCTGCG	300		
Db	5614 CGCCACACTTGGCTCCCAAAAGTCTG--GATTACAGGCTGTAACACACAGCCCTGCG	5670		
QY	301 TGCGTAATTTTGGGATGAGAAAGGGTTTCAATGATGTCGCAAGCTGCTGCTG--	357		
Db	5671 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTG	5729		
QY	358 --AGCTCAGAGTCACTGCTCAGCTCCTCCCAAGTGTGAGATTAACAGGGCTGAGC	415		
Db	5730 CCTGATCTGGATCAGTCAACCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5789		
QY	416 CGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	475		
Db	5790 CTCCCAAGTACCCAGATTAACAGGATGTCCACACACCCAGGATTAATTTTGTATTTT	5849		
QY	476 TGAAGTCAAGTGTGATATCA--CAGCTCAGTGAAGCTTCAACTCTGATGAACAG--CA	532		

Db	5850	GGTAGACACGAGGTTTACCATGTTGGCCAGCGCTGGTTTGAACCTCTGACCTCAGGTGA	5909
Qy	533	TCTCTCGCCTCAGCCTCCCAAGTAGTGGGACCAGACATGCACCTACCTGGC	591
Db	5910	TCCACCGCCCTCAGCCTCCCAAGTAGTGGGACCAGACATGCACCTACCTGGC	5969
Qy	592	-----TAAFTTTTATTTTATTTTAAATTTTGTAGACAGACTCMAACTCTGT	640
Db	5970	TCAGGAAGTATTTTATTTTAAATTTTATTTTATTTTGTAGAGAGAGTCT-TGCTGTGT	6028
Qy	641	CACCCAGGCTGAGATGCGAGTGGCCAAATCTTGGCTCACTGCACACTCTGCTCCCGGGTT	700
Db	6029	CGCCACAGCTAGATGTGACGACGAGGATCTCGCTCACTGCAGACTCCGCCCCAGATT	6088
Qy	701	CAGTATATCTCTGCCCCAGCCTCTGAGTAGCTGGGAGTACAGCGC--CCACGACG	757
Db	6089	CAGCCATATCTCTGCCCCAGCCTCTGAGTAGCTGGGAGTACAGCGCGCCCGCACCA	6148
Qy	758	CCATGCAATTTTGTGTAATTTTAGTAGAGATGGG-GTTACACATGTTGGCCAGTTGA	816
Db	6149	CCGGCTAATTTTGTGTAATTTTAGTAGAGACGGGTTTTCACCGCTGTATGCCCCGAGGG	6208
Qy	817	TCTTGATCTCTGAGACTTGTGATGTCGCTGCGCTGCCCAAGTGCATGGATTTACAG	876
Db	6209	TCTTGATCTCTGAGACTGATGATGTCGCTGCGCTGCCCAAGTGCATGGATTTACAG	8288
Qy	877	GCGTAGCCACACAGCGCGCGCTATTTTAAATTTTGTGTTGAATGGAACTCTCACT	936
Db	6269	GTCGAGACCCACACACCGCGCT-----ATTTTTATTTTGTGTAAGAGAGCTCACT	6320
Qy	937	CTGTACCACAGCTGAGAGTGCATATGCCAAATCTGGCTCACTGCAACTCTGCTCCG	996
Db	6321	CTGTACCCTGGGCTGAGAGTGCATATGCCAAATCTGGCTCACTGCAACTCTGCTCCG	6379
Qy	997	GGCTCAGAGCAATTTCTGCTGTCTGACCTCCACACAGCTGGGATTTAGGGGACCTGCGAC	1056
Db	6380	AGCTCAAGTATCTCTCCACCTCACTCTCAACAGTAATTTGGAGCTACAGGGACACCCAC	6439
Qy	1057	CACACCCCGCATTTTGTAT-----TTTCATATGAGGGGGGTTTTCAC	1101
Db	6440	CATGCCACACATTTATTTATTTATTTATTTATTTATTTTCATATGAGATGAGGCTCC	6499
Qy	1102	CATTTTGTAGAGCTGGTCTCAAACTCTGACCTCAGAGTACCCACCTGCTCAGCTTC	1161
Db	6500	TGTGTTCTCAGAGCTGGTCTTGAACCTCTGAGCTCAGGGGATCCTTGTGCTGGGCTCC	6559
Qy	1162	CAGAGTCTGGGATTTACAGGCTGAGGCACTCAACGAGCGGCTAATTTAGATAAA	1218
Db	6560	CAGAGTCTGGGATTTACAGGCTGAGGCACTCAACGAGCGGCTAATTTAGATAAA	6616

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: RESULT 11
: US-09-496-694B-3
: Sequence 3, Application US/09496694B
: Patent No. 6335194
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: APPLICANT: Elizabeth J. Ackermann
: APPLICANT: Eric E. Swazey
: APPLICANT: Lex M. Cosvert
: TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
: FILE REFERENCE: ISPH-0439
: CURRENT APPLICATION NUMBER: US/09/496,694B
: CURRENT FILING DATE: 2000-02-02
: PRIOR APPLICATION NUMBER: 09/286,407
: PRIOR FILING DATE: 1999-04-05
: PRIOR APPLICATION NUMBER: 09/163,162
: PRIOR FILING DATE: 1998-09-29
: NUMBER OF SEQ ID NOS: 249
: SEQ ID NO 3
: LENGTH: 14796
: TYPE: DNA
: ORGANISM: Homo sapiens

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1  FEATURE:
2  NAME/KEY: CDS
3  LOCATION: (2811)...(2921)
4  NAME/KEY: CDS
5  LOCATION: (3114)...(3283)
6  NAME/KEY: CDS
7  LOCATION: (5158)...(5275)
8  NAME/KEY: CDS
9  LOCATION: (11955)...(12044)
10
11 JS-09-456-694B-3

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Query Match	33.0%;	Score 475.4;	DB 4;	Length 14796;
Best Local Similarity	69.8%;	Pred. No. 7.8e-123;		
Matches 877;	Conservative	0;	Mismatches 321;	Indels 59; Gaps 15

OY	1	TTTTTTTTTGGAGTGGAGTTTGGCTTGGCTTTGGCCAGCGGTGAGTGGCAATGGCGCA	60
Db	5380	TTTTTTTTTCTGACAGTATAG--TTTCACCTCTGTTGGCCAGCGGTGAGTGGCAATGGCTGCA	5438
OY	61	TCCTCAGCTCACCGCAACCTCCGCGCTCCCGGGTTCAAGGATTTCTGCTCCACAGCTCC	120
Db	5439	TCCTGGCTCAGTGCACACCTCTGCGCTCTCGGGTTCAAGATTTCTCTGCTCCAGCTCC	5498
OY	121	CAGTACGCTGGGATTAACAGGCATGTGACACCCACGCTCGGCTAATTTTGTATTTT	180
Db	5499	AAGTAACGGGATTAACAGGAAGTCCACACACCCACCTAATTTT---TGTATTTT	5555
OY	181	TAGAGATGAGATTTCTCCATGTGTGGTGGGCGGTCTGAGATCCCGACCTCAGATGATC	240
Db	5556	TAGAGATGGGTTTACACCAATTTGCCAGGGCTGGTCTGAACTCTGACCTC--GTGATT	5613
OY	241	CCCTCGTCTCGGCGCTCCCAAGTGTCTAATACAGACATCGGCACCATCCCGGCTCTCC	300
Db	5614	CGCCACACTTGGCGCTCCCAAGTGTG--GATTACAGGGGTGAACACACAGCGCTGG	5676
OY	301	TGCGTAATTTTGTGTGTAAGAAAGGTTTCACTGATGTGCCCAAGCTGTCTCTG---	357
Db	5671	TTTTTTTTTTTGTGTC--GAGACACAGTTTCACTCTGTACCACAGCTGGAGTAGGTCG	5728
OY	358	--ACTCAGAGATCCACCTGCTGCGCTGCCCAAGTGGTGGATTTACAGCGTGGAC	415
Db	5730	CCTGATCTCGGATCACTGCACACCTCGGCTCTGGGCTCAAGTGTATGCTGCTTCAC	5788
OY	416	CGTGCCTGGCCTTTTATTTATTTTATTTTAAAGACACAGTGTCTCCACTCTTACCAGGA	475
Db	5790	CTCCAGATGACCGAGATTACAGGATGTGCACACACCAAGTAATTTTGTATTTT	5843
OY	476	TGAAGTCAGTGTGTGATCA--CAGCTACCTGACGCTTCACTCTGAGATCAAG--CA	532
Db	5850	GGTAGAGACGAGTTTACCAATGTTGGCCAGGCTGGTTTGAATCTCGACCTCAGTGA	5908
OY	533	TGCTCTGCGCCAGCGCTCCCAAGTAGTGGGGCCAAACATATGCACCACTACACCTGGC-	591
Db	5910	TTCAACCGCGCTCAGCTCCCAAAAGTGTGAATTTATAGGTGTGAACCAACACCTGGCC	5965
OY	592	-----TAAATTTTATTTTATTTTAAATTTTATTTTGAAGACAGATCTCAACTGT	640
Db	5970	TCAGAGATATTTTATTTTAAATTTATTTATTTATTTTGAATGATGATCT--TGTCTGT	6022
OY	641	CACCCAGGCTGAGTCACTGAGTGGCGCAATCTTGGCTCACTGCACACCTGTGCCGGGT	700
Db	6029	CGCCAGGCTGAGATGACGACGCGGATCTCGGCTCACTGCACAGCTCCGCCCCAGGTT	6088
OY	701	CAAGTTATTCCTCGCCCGACGCTCTGATGATGAGTGGGACATCAAGGGC---CCACACG	757
Db	6089	CAACCATCTCTGCTCAGCTCCCGACGATGAGTGGGACATCAAGGGC---CCGCCACA	6148
OY	758	CCTAGCTAATTTTGTATTTTATTTAGTAGAGATGG--GTTCACATCTTTCGCCAGGTGA	816
Db	6149	CCCGGCTAATTTTGTATTTTATTTAGTAGAGACGGGTTTCAACCTGTATACCAAGAGG	6206
OY	817	TCCTTATCTCGAACCTTGTGATCTGCGCTCGGCTCCCAAGTGTCTGGATTTACAG	876


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; CURRENT APPLICATION NUMBER: US/09/978,197
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/813,817
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 59065
; TYPE: DNA
; ORGANISM: Human
US-09-978-197-3

Query Match      28.9%; Score 416.4; DB 4; Length 59065;
Best Local Similarity 67.7%; Pred. No. 4.3e-106;
Matches 815; Conservative 0; Mismatches 326; Indels 63; Gaps 14;

QY 42 CTGGGTGCAATGGGGCAATCTCAGCTCAGCCGCAACCTCCCGCTCCGGGTCAAGCAT 101
DB 15163 CTGGAGGCGAGTGGCGCATCTCAGCAGACATGCAACCTCCATCTCCAGGTTCAAGCTAT 15104
QY 102 TCTCTGCTCAGCTCCCGCAGTACGTGGATTTACAGCATATGACACCCAGCTCGGCTA 161
DB 15103 TCTCTGCTCAGTCTCTAGTACTGAGTTACAGGTGGCTGGCATCTGCTGCTGCTA 15044
QY 162 ATTTTGTATTTTATTTTATGAGATGAGATTTCTCATATGTTGGTACGCTGCTCGAA 221
DB 15043 ATTTT---TGTATTTTATGATAGAGACAAGGTTTCCACATGTTGGCGAGGCTGCTGGA 14987
QY 222 CTCCGACCTCAGATATCCCTCCGCTCGGCGCTCCCAAGGCT-ACATACAGACATGG 280
DB 14986 CTCCGACCTCAGGATATCCGCGCGCTCGACCTCCCAAGGCTGGGATTTACAGGCGCG 14927
QY 281 CCACCATCCCGGCTCTGCTGCTAATTTTGTGTGTAAGAAACAGGTTTCACTGATGTG 340
DB 14926 AGCCAGCGCGCCAACTCCATTTTTTTTTTGAAGACAGTCTTGCTGTGCG 14867
QY 341 CCCAAGCTG-----GTCCTGAGCTCA 363
DB 14866 CCCAAGGCTGAGATGCGAGTGGCGCATCTCAGCTCAGCTCAGCTCCGCTCCGCGGTCA 14807
QY 364 AGCAGTCCAGCTGCTCAGCTCCCAAGTGTGGGATTTACAG--GCGTGCAGCGCTGCC 421
DB 14806 CGCATTCTCGCTCAGCTCAGCTCCGAGTACGAGGAGCTACAGGTCCTGCACCATCCTC 14747
QY 422 TGGCTTTTATTTTATTTTATTTTAAAGACAGAGTGTCCACTTTACCAAGATGAGT 481
DB 14746 TGGCTAATTTTGTATTTTATTTAGTAGACGCGGTTTACGTGTGTAGCAGGATGCT 14687
QY 482 GCAAGTGTGTATCAGACTCAGCTCAGCTTCAACTCCTGAGATGAAGCATCTCTGTC 541
DB 14686 -GCAATCTCTGACCTTGTGATCCGCCCTCGGCTCCCAAGAGTGTGGATTTACATGC 14628
QY 542 CTCAGCCCTCCAGATGCTGGGACCAAGA-----CATGCACACTACACCTGGCTAAT 596
DB 14627 GTAGCCACCGCTGCTGCGCTCCATATTTTATTTTATTTTATTTTATTTTATTTT 14568
QY 597 TTTATTTTATTTTATTTTATTTTGAAGACAGATCTCAACTGTACACCGAGCTGAGAT 656
DB 14567 TATTTTATTTTATTTTATTTATTTAGACAGACTCTC-CTCTGTCTCTCCAGGCTGAGAT 14509
QY 657 CAGTGGCCCAATCTTGGCTCAGCTCAGCTGCTCCCGGGTTCAGATTTCTCTGTC 716
DB 14508 CAGTGCATGATGTTGGCCCACTGCAACCTCGCTCTGGGTTCAAGCGATTCGTCG 14449
QY 717 CCCAGCTCTCC---TGAGTAGCTGGGACTACAGGGCC---CCACCAAGGCTAGCTATTT 770
DB 14448 CTCAGCTCTCCAGTAGTAGAGTGGGACTACAGGACATGCAACCTAGCTGCTGCTA--TT 14391
QY 771 TTTTATTTTATTTAGTAGAGATGGG--TTCCACATGTTCCAGAGTGTGATTTGATTTCTGG 829
DB 14390 TTTGATTTTTCAGTAGATGGGTTTACACATGTTGGCCAGGCTAGTCTCATCTCTCTG 14331
QY 830 ACCT--TGTGATCTGCTGCTCGGCTCCCAAGAGTGTGGGATTTACAGGCGTGAAGCAC 887
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DB 14330 ACCTCAAGTATATCCACCTGCGCTTGGCTCCCAAAAGTGTGGATATCTGCGGTGAGCAAA 14271
QY 888 CAGCGCGGCTATTTT-TTAAATTTTGTGTTGAATNGAATCTCACTCGTATACCA 946
DB 14270 CCGGCTGCTGCTGTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 14211
QY 947 GCGTGGAGTGCATATGGCCAAATCTCGGCTCAGCTCAGCACTGCTCCCGGAGCTCAAGCG 1006
DB 14210 GCGTGGAGTGTAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 14151
QY 1007 ATTTCTGCTCAGCTCTCCCAAGCAGCTGGGATTTAGGGGACCTGCGACCAACACCGCC 1066
DB 14150 ATCTCTGCTCAGCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 14091
QY 1067 TAAATTTTGTATTTTATTTATTAAGGCGGGTTCACCATATTTGTACAGGCTGTC-TCAA 1125
DB 14090 TAAATTTTGTATTTTATTTTGTGGGATGATGATGATGATGATGATGATGATGATG 14031
QY 1126 CTCTGACCTCAGTGCAGCCACCTGCTCAGCTTCCAAAGTGTGGGATTTACAGGCTG 1185
DB 14030 CTCTGAGTTCAAGCAATCTCTCCGCTAGAGGCTCTCCCAAGTGTGATTTATAGTGT 13971
QY 1186 AGCC 1189
DB 13970 AGCC 13967

RESULT 14
US-09-735-934A-3/c
; Sequence 3, Application US/09735934A
; Patent No. 6372468
; GENERAL INFORMATION:
; APPLICANT: Li, Jieyin et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CLO00851
; CURRENT APPLICATION NUMBER: US/09/735,934A
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 43950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-934A-3

Query Match      28.6%; Score 412.2; DB 4; Length 43950;
Best Local Similarity 66.0%; Pred. No. 5.6e-105;
Matches 863; Conservative 0; Mismatches 333; Indels 111; Gaps 14;

QY 2 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 61
DB 37294 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 37235
QY 62 CTCAGCTACCGCAACCTCCG--CTCCGCGGTTCAAGGATTTCTCTGCTCAGCTGCC 120
DB 37234 CTCGCTACCGCAACCTCTCCGCTCTGCTGCTTCAAGCAATTTCTCTCTCAGCTCCT 37175
QY 121 CAGTAGCTGGGATTTACAGGCAATGTGACACCAAGCTCGGCTAATTTTATTTTATTTTATTT 180
DB 37174 GAGAACCTGGGATTTACAGGCTTCCGCAACATGCGCCAGCTAATTTT---TGTATTTTAG 37118
QY 181 TAGAGATGAGTGTCTCATGTTGTGTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 37117 TAGAGACGGGTTTGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 37058
QY 241 CTTCTGCTCGGCTCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 37057 TGGCGGCTCAGACCTCCCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 37002
QY 301 TGGCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 360
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Db 37001 CCAGAAACTTTTAAATATGTTTGGACAACTTGGGACATGCAATATTTTCCCAACTG 36942
QY 361 TCAGACAGTCCAGCTGCTGAGCTCCCAAGTCTGGGATTAAGAGCGCTGACCGTGC 420
Db 36941 TTAATACACACAGATTTTG-----AAGACATAGTAAAGAAAACCAACAATGTT 36892
QY 421 CTGACCTTTTATTTTATTTTATTTTAAAGACACAGTGTCCACCTTACCAGGATGAAG 480
Db 36891 TCATTGAGTTTGTGTTCTTTTAAAGACAA-GGGTCTGTCTGTCTGACCCACTGAG 36833
QY 481 TCAGATGCTGTATACAGCTCACTGACGCTTCACTCTGAGATCAAG-CATCTCTCT 539
Db 36832 TCAGATGCTGTATACAGCTCACTGACGCTTCACTCTGAGATCAAG-CATCTCTCT 36773
QY 540 GCTTACGCTTCCCAAGTGTGGGACCAAGACATGACCACTGACCTGCG----- 591
Db 36772 ATCTTGGCTCCCAAGTGTGGGATTAAGGACATGACCACTGCGCTTAAATAA 36713
QY 592 ----- 591
Db 36712 TTTTATGCTGACTACATGTTGAATAAGTCTATGCTTGGATTAACATATATATAT 36653
QY 592 TAAATTTTATTTTATTTTATTTTATTTTGAAGACAGAGTCTC-----AACTCTGTCAC 644
Db 36652 ATATATATATATTTTATTTTATTTTATTTTGAAGACAGAGTCTGCTGCTGCTGTCAC 36593
QY 645 CAGGCTGAGTACAGTCCGCAATCTTGGCTCACTGACGCTGCTGCTGCTGCTGCTGCTGCT 704
Db 36592 CAGGCTGAGTACAGTCCGCAATCTTGGCTCACTGACGCTGCTGCTGCTGCTGCTGCTGCT 36533
QY 705 TTAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 761
Db 36532 CCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36473
QY 762 GCTAA--TTTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 818
Db 36472 GCTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 36413
QY 819 TTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
Db 36412 TCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36353
QY 879 GTGAGCCACAGCGCCGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 938
Db 36352 GTGAGCCACAGCGCCGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 36298
QY 939 GTTACCCAGGCTGAGTGCATGCGCAATCTGCGCTCACTGCACTCTGCTGCTGCTGCTGCTGCT 998
Db 36297 GTTATTCAGGCTGAGTGCATGCGCAATCTGCGCTCACTGCACTCTGCTGCTGCTGCTGCTGCT 36238
QY 999 CTCACGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1058
Db 36237 CTCACGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36178
QY 1059 CACCCGCTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1115
Db 36177 TTCCGCGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 36118
QY 1116 TGGTCTCAACTCTGACCTCAAGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1175
Db 36117 TGGTCTCAACTCTGACCTCAAGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160
QY 1176 TACAGCGCTGAGCACTGACCAAGCGGCTAATTTATTAATAAAAA 1222
Db 36059 TACAGCGCTGAGCACTGACCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36013

RESULT 15
US-08-687-080-101/c
Sequence No. 101, Application US/08687080
Patent No. 5965427
GENERAL INFORMATION:

APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111.30
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 5543 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 3' END OF INTRON 19 OF RAD50 GENOMIC
INDIVIDUAL ISOLATE: SEQUENCE
US-08-687-080-101
Query Match 27.8%; Score 400.8; DB 2; Length 5543;
Best Local Similarity 72.1%; Pred. No. 3.5e-102;
Matches 610; Conservative 0; Mismatches 217; Indels 19; Gaps 6;
QY 592 TAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 651
Db 1274 TGACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1216
QY 652 GAGTGCAGTGGCGCAATCTTGGCTCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 711
Db 1215 GAGTGCAGTGGCGCAATCTTGGCTCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1156
QY 712 CCTGCCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768
Db 1155 CCTGCCCGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
QY 769 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 827
Db 1095 TTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1036
QY 828 GGACCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
Db 1035 TGACCTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 976
QY 888 CAGCGCGGCTTAT-----TTTAAATTTTGTGTTTGAATGGAATCTCACTC 937
Db 975 CAGCGCGGCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 916
QY 938 -TTTATCCAGGCTGAGTGCATGCGCAATCTGCGCTCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 996

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Db 915 TTGTACCCAGGCTGAAGTGCATGATGATCTCGGCTCACTGCATCTCTGCTCCCA 856
Oy 997 GGCTCAAGCGATTCCTCCCTGCTCAGCCCTCCACAGAGCTGGATTAAGGCGACCGCCAC 1056
Db 855 GGTTCAGAGCGATTCCTCGCTCAGCCCTCTGAGTACCTGGATTACAGCGCGGTCTAC 796
Oy 1057 CACACCCCGCTAATTTTGTATTTTCATTTAGAGCGGGGTTTCACCAATATTGTGAGGCT 1116
Db 795 CACACCGTGGCTAATTTTCTATTTTCATAGATAGATGGGTTTACATATTGGCCAGGCT 736
Oy 1117 GGCTCAAACTCTGAGCTCAGTGACCCACCTGCTCAGCTTCGCAAGTGTGGATT 1176
Db 735 AGTCTTGAACCTCTGAGCTCAGTGATCCGCTGCTGGCTCCCAAGTGTGGGATT 676
Oy 1177 ACAGGCGTGAAGCGCTCAGCCAGCCGCTAATTTAGATAAATAATATGTAGCAATGGG 1236
Db 675 ACAGGCAATGAGTCACTGCGCTGGCTCTCTCTTTATTTGACTAGTAATCTTCACGA 616
Oy 1237 GGGTCTTGCTATGTTGCCAGGCTGCTCAAACTTCTGCTCATGCAATCTTCCAAA 1296
Db 615 AGCATATCAGACTTCATGCAATCTTTTATACACTCT--CTCGTGTTCATTACTT 559
Oy 1297 TGAGCCACACAGCCAGGCACTCATATTTTAAACAGTTACATCTTATTAGTATAC 1356
Db 558 CTGCCCCCTATTCTACACTGCTGTTTCCCATTAATTGAATAATCATTTATCTTGC 499
Oy 1357 TAGAAGTAAATACATAAATGTCAAACCTGCAAAATTCAGTATGACAGAGTCTTTTA 1416
Db 498 TCTATTTATTAATTAAGTAAATTAATTTCTGAAACAAGAGTTACAAAGTAAACTTAA 439
Oy 1417 TAACTT 1422
Db 438 TACCAT 433
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Search completed: July 20, 2003, 07:55:10
Job time : 83 secs

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